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OM protein - protein search, using SW model

Run on: June 9, 2005, 16:27:48 ; Search time 116.174 Seconds

(without alignment)
1245.097 Million cell updates/sec

Title: US-10-791-166-2

Perfect score: 1970

Sequence: MLSTSRSPFIRNTNESGEEV.....GKGSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:
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 3: geneseqP2000s:
 4: geneseqP2001s:
 5: geneseqP2002s:
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DR N-PSDB; AAQ96297.
 XX DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
 PT for identifying antagonists and for treating diseases characterised by
 PT monocytic infiltrates.
 XX

Claim 2; Fig 1; 84pp; English.

XX To identify and clone new members of the chemokine receptor gene family,
 CC degenerate oligo primers were designed corresp. to the conserved
 CC sequences R79167 in the second and R79168 in the third transmembrane
 CC domains of the MCP-1alpha/BANTES receptor, the IL-8 receptors and the
 CC HOMSTRS orphan receptor (GenBank Accession #M9293. The degenerate oligo
 CC incorporating EcoRI and XbaI sites at their 5' ends are Q96299 and
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers
 CC yielded a number of PCR products. One cDNA appeared to encode a novel
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA
 CC library was constructed in pPROG and probed with the PCR product. A 2.1
 kb cDNA clone was obtnd. Analysis of additional clones in the MM6 cDNA
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA
 CC sequence first obtnd. from the 5' UTR through the putative seventh
 CC transmembrane domain but contained a different cytoplasmic tail. The
 CC second sequence appears to represent alternative splicing of the carboxy-
 CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-
 CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-
 CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.
 CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 374 AA;

SQ Score 1970; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 5.1e-15; Mismatches 0; Indels 0; Gaps 0;

Matches 374; Conservative 0; Gaps 0;

Qy 1 MLSTSRSPRTNTNSGREGVTTFEDYDYGAPCHKFDVKQIGAQOLLPPLYSLVPIFGFVGNN 60

Db 1 MLSTRSRSPRTNTNSGREGVTTFEDYDYGAPCHKFDVKQIGAQOLLPPLYSLVPIFGFVGNN 60

Qy 61 MLVVLILINCKLKCLTDIYLNLASIDPLLELTLPWAHSAANEWFGNAMCKLFTGLY 120

Db 61 MLVVLILINCKLKCLTDIYLNLASIDPLLELTLPWAHSAANEWFGNAMCKLFTGLY 120

Qy 121 HIGYFGGGIFFILLTIDYLAIVHAFALKARTVTFGVTVTSVTLVAVFASVPGIIFTK 180

Db 121 HIGYFGGGIFFILLTIDYLAIVHAFALKARTVTFGVTVTSVTLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVTYVCGPYFPGRMNFFTMRLNLLGVLPLLMIVCYSGILKLRLCRNEKGRHR 240

Db 181 CQKEDSVYVCGPYFPGRMNFFTMRLNLLGVLPLLMIVCYSGILKLRLCRNEKGRHR 240

Qy 241 AVRVTIMIVYFLWTPYNIIVLNTQEFFGLSNCESTSOLDQATQVTTETLGMTHCCCI 300

Db 241 AVRVTIMIVYFLWTPYNIIVLNTQEFFGLSNCESTSOLDQATQVTTETLGMTHCCCI 300

Qy 301 NPIIYAFVGBKPSLSEFHLAGCRIAPILOKPVCGSGPGRPKRNKVTOGLLDRGKGSKI 360

Db 301 NPIIYAFVGBKPSLSEFHLAGCRIAPILOKPVCGSGPGRPKRNKVTOGLLDRGKGSKI 360

Qy 361 GRAPEASLQDGKEGA 374

Db 361 GRAPEASLQDGKEGA 374

Qy 751 COKEDSYVCGEKFPLLITDYLAIYHAFALKARTVTFGVTVTSVTLVAVFASVPGIIFTK 180

Db 751 COKEDSYVCGEKFPLLITDYLAIYHAFALKARTVTFGVTVTSVTLVAVFASVPGIIFTK 180

Qy 121 HIGYFGGGIFFILLTIDYLAIVHAFALKARTVTFGVTVTSVTLVAVFASVPGIIFTK 180

Db 121 HIGYFGGGIFFILLTIDYLAIVHAFALKARTVTFGVTVTSVTLVAVFASVPGIIFTK 180

Qy 181 COKEDSYVCGEKFPLLITDYLAIYHAFALKARTVTFGVTVTSVTLVAVFASVPGIIFTK 240

Db 181 COKEDSYVCGEKFPLLITDYLAIYHAFALKARTVTFGVTVTSVTLVAVFASVPGIIFTK 240

Qy 241 AVRVTIMIVYFLWTPYNIIVLNTQEFFGLSNCESTSOLDQATQVTTETLGMTHCCCI 300

Db 241 AVRVTIMIVYFLWTPYNIIVLNTQEFFGLSNCESTSOLDQATQVTTETLGMTHCCCI 300

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytotoxic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.
 XX

AX Homo sapiens.

OS EN WO200172830-A2.

XX

PD 04-OCT-2001.

AX 02-APR-2001; 2001WO-EP003708.

PF XX

(IPPF-) IIPP PHARM GMBH.

(FORS/) FORSSMANN U.

PA XX

PR 31-MAR-2000; 2000DB-01016013.

DR XX

WPI; 2001-626255/72.

XX

Diagnostic agent containing two or more receptor-specific ligands, useful
 for detecting tumors, inflammation etc., also therapeutic use of ligand
 inhibitors.

XX Disclosure; Page 9; 26pp; German.

PS XX

This invention describes a novel diagnostic agent (A) comprising at least
 two different ligands (1) for receptors (II) that are implicated in
 disease. (A) are used for the diagnosis of tumors (and their
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (1) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytotoxic, antiinflammatory, antiasthmatic, antiarthritic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-ARG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention

AX Sequence 374 AA;

Query Match Score 1970; DB 4; Length 374;
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;
 Matches 374; Conservatice 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MUSTRSRSPRTNTNSGREGVTTFEDYDYGAPCHKFDVKQIGAQOLLPPLYSLVPIFGFVGNN 60
 Db 1 MUSTRSRSPRTNTNSGREGVTTFEDYDYGAPCHKFDVKQIGAQOLLPPLYSLVPIFGFVGNN 60
 Qy 61 MLVVLILINCKLKCLTDIYLNLASIDPLLELTLPWAHSAANEWFGNAMCKLFTGLY 120
 Db 61 MLVVLILINCKLKCLTDIYLNLASIDPLLELTLPWAHSAANEWFGNAMCKLFTGLY 120
 Qy 121 HIGYFGGGIFFILLTIDYLAIVHAFALKARTVTFGVTVTSVTLVAVFASVPGIIFTK 180
 Db 121 HIGYFGGGIFFILLTIDYLAIVHAFALKARTVTFGVTVTSVTLVAVFASVPGIIFTK 180
 Qy 181 CQKEDSVTYVCGPYFPGRMNFFTMRLNLLGVLPLLMIVCYSGILKLRLCRNEKGRHR 240
 Db 181 CQKEDSVYVCGPYFPGRMNFFTMRLNLLGVLPLLMIVCYSGILKLRLCRNEKGRHR 240
 Qy 241 AVRVTIMIVYFLWTPYNIIVLNTQEFFGLSNCESTSOLDQATQVTTETLGMTHCCCI 300
 Db 241 AVRVTIMIVYFLWTPYNIIVLNTQEFFGLSNCESTSOLDQATQVTTETLGMTHCCCI 300
 Qy 301 NPIIYAFVGBKPSLSEFHLAGCRIAPILOKPVCGSGPGRPKRNKVTOGLLDRGKGSKI 360
 Db 301 NPIIYAFVGBKPSLSEFHLAGCRIAPILOKPVCGSGPGRPKRNKVTOGLLDRGKGSKI 360
 Qy 361 GRAPEASLQDGKEGA 374
 Db 361 GRAPEASLQDGKEGA 374

RESULT 2
 AAG80107
 ID AAG80107 standard; protein: 374 AA.

XX 17-JAN-2002 (first entry)
 XX Human CCR2a protein.

Qy	301 NPIIYAFVGEKERSLFLHIALGCRIAPILOKPVCCGPGRGVNVKVTGGLDGRGKGS1	360	Db	1 MLISSRSRFRINTNESSEBEVTTFDYDYGAPCHKFDVKIGAQOLPPLYSLVFIFGVGN 60
Db	301 NPIIYAFVGEKERSLFLHIALGCRIAPILOKPVCCGPGRGVNVKVTGGLDGRGKGS1	360	Qy	61 MLVVLILINCKLKCLDIYLNLAIISDPLFLITLPLWAHSANNEWFGNAMKLFITGLY 120
Qy	361 GRAPEASLQDKEGA 374		Db	61 MLVVLILINCKLKCLDIYLNLAIISDPLFLITLPLWAHSANNEWFGNAMKLFITGLY 120
Db	361 GRAPEASLQDKEGA 374		Qy	121 HIGYFGGIFFIILTIDRYLAIVHAFAALKARTVTFGVVTSVITWLAFAVASYPGIIFTK 180
AC	ABU09083;		Db	121 HIGYFGGIFFIILTIDRYLAIVHAFAALKARTVTFGVVTSVITWLAFAVASYPGIIFTK 180
XX	23-JUL-2003 (first entry)		Qy	181 COKEDSYVCGPYFPRGNNFTIMRNTLGLVPLLLIMVICSGILLKLRLCRNEKVRHR 240
DE	Human chemokine receptor-2 (CKR-2) polypeptide.		Db	181 COKEDSYVCGPYFPRGNNFTIMRNTLGLVPLLLIMVICSGILLKLRLCRNEKVRHR 240
XX			Qy	241 AYRVIFITMIVFLFWTPYNNVILNTFOEFFPQLSNGESTSOLDQATQVTEITGMTHCCI 300
KW	Human; thymus expressed chemokine: TBCK; chemokine; MIP-3alpha; receptor; MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma; monocyte/dendritic cell receptor for chemokine; inflammatory condition; abnormal physiology; abnormal proliferation; degeneration; atrophy; antiinflammatory; antiasthmatic; cytostatic; chemokine receptor-2; CKR-2.		Db	241 AYRVIFITMIVFLFWTPYNNVILNTFOEFFPQLSNGESTSOLDQATQVTEITGMTHCCI 300
KW	Homo sapiens.		Qy	301 NPIIYAFVGEKERSLFLHIALGCRIAPILOKPVCCGPGRGVNVKVTGGLDGRGKGS1 360
PP	OS		Db	301 NPIIYAFVGEKERSLFLHIALGCRIAPILOKPVCCGPGRGVNVKVTGGLDGRGKGS1 360
XX	US2003018167-A1.		Qy	361 GRAPEASLQDKEGA 374
PD	23-JAN-2003.		Db	361 GRAPEASLQDKEGA 374
XX	03-JAN-2002; 2002US-00039659.		XX	
PP			AC	ADD44861;
XX			AC	ADD44861;
PR	05-JUL-1996; 96US-0021664P.		DT	29-JAN-2004 (first entry)
PR	11-OCT-1996; 96US-0028329P.		XX	
PR	04-JUN-1997; 97US-0048593P.		DB	Human Protein P41597, SEQ ID NO 10292.
PR	03-JUL-1997; 97US-00887977.		XX	
XX	(SCHE) SCHERRING CORP.		KW	Human; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
PA	Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;		KW	
PI	XX		XX	
DR	WPI; 2003-416900/39.		OS	Homo sapiens.
XX			PN	WO2003016475-A2.
PT	New chemokines, TBCK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCR, useful for treating conditions associated with abnormal physiology or development, including inflammatory conditions (e.g. asthma), and abnormal proliferation.		PD	27-FEB-2003.
PT			XX	
PT			PF	14-AUG-2002; 2002WO-US025765.
XX			XX	
PS	Disclosure; Page 9-10; 54pp; English.		PR	14-AUG-2001; 2001US-0312147P.
XX			PR	01-NOV-2001; 2001US-0346388P.
PT	The invention relates to nucleic acids encoding the chemokines TBCK, MIP-3 alpha, MIP-3beta, DC CR and M/DC CR. The polypeptide sequences are useful in isolating DNA clones encoding the chemokines, for generating antibodies, and for predicting oligonucleotides for screening a library to isolate species variants. A nucleic acid encoding a chemokine polypeptide can be used to identify genes, mRNA and cDNA species which encode related or homologous ligands, as well as DNA encoding homologous proteins from different species. The chemokines and antibodies which bind to the polypeptides are useful in the treatment of conditions associated with abnormal physiology or development, including inflammatory conditions such as asthma, abnormal proliferation, regeneration, degeneration and atrophy. This sequence represents the human chemokine receptor-2 (CKR-2) polypeptide, used in the scope of the invention		PR	26-NOV-2001; 2001US-0333347P.
CC	Sequence 374 AA;		XX	XX
CC	Query Match 100.0%; Score 1970; DB 6; Length 374;		PA	(GEHO) GEN HOSPITAL CORP.
CC	Best Local Similarity 100.0%; Pred. No. 5.1e-215;		PA	(PARB) BAYER AG.
CC	Mismatches 0; Indels 0; Gaps 0;		XX	New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
CC	MLSTSRSPRINTNESSEBEVTTFDYDYGAPCHKFDVKIGAQOLPPLYSLVFIFGVGN 60		PT	WPI; 2003-268312/26.
CC			XX	DR GENBANK; P41597.
CC			PS	Claim 1; Page; 101pp; English.
CC			XX	The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also CC claimed are a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a nucleotide sequence CC which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC the sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 374 AA;

Query Match	100.0%	Score 1970;	DB 7;	Length 374;
Best Local Similarity	100.0%	Pred. No. 5.1e-215;		
Matches 374;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Qy 1 MLLTSRSPRINTNESGEVTTFFDYGAPCKFDKFDYQIGQLPPLYSLVIFGVGN 60
Db 1 MLLTSRSPRINTNESGEVTTFFDYGAPCKFDKFDYQIGQLPPLYSLVIFGVGN 60
Qy 61 MLVVLILINCGLKCLTDIYLNLAIISDLFLITLPLWAHSANNEWFGNAMCKLFTGly 120
Db 61 MLVVLILINCGLKCLTDIYLNLAIISDLFLITLPLWAHSANNEWFGNAMCKLFTGly 120
Qy 121 HIGYFGGIFTIILTIDRYLAIVHAFALKARTVTFGVVTSTVTLVAVPAASPVGIFTK 180
Db 121 HIGYFGGIFTIILTIDRYLAIVHAFALKARTVTFGVVTSTVTLVAVPAASPVGIFTK 180
Qy 181 CQEDSVYVCGPYPPRGNNFIMRNLLGVLPLLMIVCYSGLKLRLCRNEKCRHR 240
Db 181 CQEDSVYVCGPYPPRGNNFIMRNLLGVLPLLMIVCYSGLKLRLCRNEKCRHR 240
Qy 241 AYVIFTIMIVYLFWTPYNIVVLLTFOEFLSNCESTSOLDQATQVTLGMTHCCI 300
Db 241 AYVIFTIMIVYLFWTPYNIVVLLTFOEFLSNCESTSOLDQATQVTLGMTHCCI 300
Qy 301 NPIYAFYGEKFRSLFHIALGRCAPILOPKVCCGPYTRPGKVKVTOGLDGRGKRSI 360
Db 301 NPIYAFYGEKFRSLFHIALGRCAPILOPKVCCGPYTRPGKVKVTOGLDGRGKSI 360

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SQ 361 GRAPEASLQDEKEA 374

DB 361 GRAPEASLQDEKEA 374

RESULT 5
 ADD44865 ID ADD44865 standard; protein; 374 AA.
 XX AC ADD44865;
 XX DT 29-JAN-2004 (first entry)

XX Human Protein P41597, SEQ ID NO 10296.
 DE Human; pain; neuronal tissue; gene therapy;
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 OS WO2003016475-A2.

PN 241 AYVIFTIMIVYLFWTPYNIVVLLTFOEFLSNCESTSOLDQATQVTLGMTHCCI 300

XX PD 27-FEB-2003.
 XX PP 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346312P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX PI Woolf, C, D'urso, D, Befort, K, Costigan, M;
 XX DR WPI; 2003-268312/26.
 DR GENBANK; P41597.
 XX PT New composition comprising two or more isolated polypeptides, useful for
 preparing a medicament for treating pain in an animal.
 XX PS Claim 1; Page; 1017pp; English.
 XX AJX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC the sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 374 AA;

Query Match	100.0%	Score 1970;	DB 7;	Length 374;
Best Local Similarity	100.0%	Pred. No. 5.1e-215;		
Matches 374;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Qy 1 MLLTSRSPRINTNESGEVTTFFDYGAPCKFDKFDYQIGQLPPLYSLVIFGVGN 60
Db 1 MLLTSRSPRINTNESGEVTTFFDYGAPCKFDKFDYQIGQLPPLYSLVIFGVGN 60
Qy 61 MLVVLILINCGLKCLTDIYLNLAIISDLFLITLPLWAHSANNEWFGNAMCKLFTGly 120
Db 61 MLVVLILINCGLKCLTDIYLNLAIISDLFLITLPLWAHSANNEWFGNAMCKLFTGly 120
Qy 121 HIGYFGGIFTIILTIDRYLAIVHAFALKARTVTFGVVTSTVTLVAVPAASPVGIFTK 180
Db 121 HIGYFGGIFTIILTIDRYLAIVHAFALKARTVTFGVVTSTVTLVAVPAASPVGIFTK 180
Qy 181 CQEDSVYVCGPYPPRGNNFIMRNLLGVLPLLMIVCYSGLKLRLCRNEKCRHR 240
Db 181 CQEDSVYVCGPYPPRGNNFIMRNLLGVLPLLMIVCYSGLKLRLCRNEKCRHR 240
Qy 241 AYVIFTIMIVYLFWTPYNIVVLLTFOEFLSNCESTSOLDQATQVTLGMTHCCI 300
Db 241 AYVIFTIMIVYLFWTPYNIVVLLTFOEFLSNCESTSOLDQATQVTLGMTHCCI 300
Qy 301 NPIYAFYGEKFRSLFHIALGRCAPILOPKVCCGPYTRPGKVKVTOGLDGRGKRSI 360
Db 301 NPIYAFYGEKFRSLFHIALGRCAPILOPKVCCGPYTRPGKVKVTOGLDGRGKSI 360

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SQ Sequence 374 AA;

Query Match	100.0%	Score 1970;	DB 7;	Length 374;
Best Local Similarity	100.0%	Pred. No. 5.1e-215;		
Matches 374;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Qy 1 MLLTSRSPRINTNESGEVTTFFDYGAPCKFDKFDYQIGQLPPLYSLVIFGVGN 60
Db 1 MLLTSRSPRINTNESGEVTTFFDYGAPCKFDKFDYQIGQLPPLYSLVIFGVGN 60
Qy 61 MLVVLILINCGLKCLTDIYLNLAIISDLFLITLPLWAHSANNEWFGNAMCKLFTGly 120
Db 61 MLVVLILINCGLKCLTDIYLNLAIISDLFLITLPLWAHSANNEWFGNAMCKLFTGly 120
Qy 121 HIGYFGGIFTIILTIDRYLAIVHAFALKARTVTFGVVTSTVTLVAVPAASPVGIFTK 180
Db 121 HIGYFGGIFTIILTIDRYLAIVHAFALKARTVTFGVVTSTVTLVAVPAASPVGIFTK 180
Qy 181 CQEDSVYVCGPYPPRGNNFIMRNLLGVLPLLMIVCYSGLKLRLCRNEKCRHR 240
Db 181 CQEDSVYVCGPYPPRGNNFIMRNLLGVLPLLMIVCYSGLKLRLCRNEKCRHR 240
Qy 241 AYVIFTIMIVYLFWTPYNIVVLLTFOEFLSNCESTSOLDQATQVTLGMTHCCI 300
Db 241 AYVIFTIMIVYLFWTPYNIVVLLTFOEFLSNCESTSOLDQATQVTLGMTHCCI 300
Qy 301 NPIYAFYGEKFRSLFHIALGRCAPILOPKVCCGPYTRPGKVKVTOGLDGRGKRSI 360
Db 301 NPIYAFYGEKFRSLFHIALGRCAPILOPKVCCGPYTRPGKVKVTOGLDGRGKSI 360

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XX	09-SEP-2003;	2003WO-US028226.	Db	181	COKESTVYVCGPYPFRGANNFTIMRNILGVPLLLIVCYSGILKTLRNRNEKRHR	
PP			Qy	241	AVRIFTIMIVYFELNTPYNIVLILNTQEFGLSNCESTSDQDAAQTVETPLGMTCI	
XX	09-SEP-2002;	2002US-040930P.	Db	241	AVRIFTIMIVYFELNTPYNIVLILNTQEFGLSNCESTSDQDAAQTVETPLGMTCI	
PR	09-APR-2003;	2003US-0461329P.	Db	241	AVRIFTIMIVYFELNTPYNIVLILNTQEFGLSNCESTSDQDAAQTVETPLGMTCI	
XX			Qy	301	NPIIAYGEKERSLFLHALGRIAPKPVCGGPGRPGKQKVUTTQGLDGRGKSKI	
PA	(PRIM-)	PRIMAL INC.	Db	301	NPIIAYGEKERSLFLHALGRIAPKPVCGGPGRPGKQKVUTTQGLDGRGKSKI	
XX	Gaitanaris GA,	Bergmann JE,	Gragerov A,	Hobmann J,	Lil P;	
PI	Madisen L,	McIlvain KL,	Pavlova MN,	Vassilatis D,	Zeng H;	
XX	WPI:	2004-390329/36.	Qy	361	GRAPEASLQDKEGA 374	
DR	N-PSDB;	ADO9829.	Db	361	GRAPEASLQDKEGA 374	
XX	PT	Novel mammalian G protein coupled receptors, useful for identifying	RESULT 8			
PT	compounds that modulates diagnosing and treating disease condition	ADQ67847 standard; protein; 374 AA.				
PT	associated with GPCR dysfunction e.g. autoimmune diseases, angina	ID ADQ67847				
XX	pectoris, Parkinson's disease.	XX				
XX	Claim 151; SEQ ID NO 322; 542pp; English.	XX				
PS	The invention relates to human and mouse G protein-coupled receptors	DT 07-OCT-2004 (first entry)				
XX	CC (GPCRs) and nucleic acids encoding them. The invention also relates to	XX				
CC	sequences at least 90% identical to the GPCR proteins and nucleic acids	DE Human chemokine receptor CCR-2.				
CC	of the invention; methods of treating, preventing or diagnosing diseases	XX				
CC	associated with GPCRs of the invention; methods of screening for	XX				
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	XX				
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	XX				
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	XX				
CC	from the transgenic mice; kits comprising several mice, each of which has	XX				
CC	a mutation in a different GPCR gene of the invention; and kits comprising	OS Homo sapiens.				
CC	probes which hybridise to GPCR polynucleotides and vectors	XX				
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may	XX				
CC	be used in the diagnosis, treatment or prevention of a wide variety of	PN 15-JUL-2004.				
CC	diseases including neurological disorders (e.g., Alzheimer's disease,	XX				
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);	PF 09-JAN-2004; 2004US-00754471.				
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	XX				
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	PR 05-JUL-1996; 96US-0021664P.				
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	PR 11-OCT-1996; 96US-0028349P.				
CC	from the transgenic mice; kits comprising several mice, each of which has	PR 04-JUN-1997; 97US-004853P.				
CC	a mutation in a different GPCR gene of the invention; and kits comprising	PR 03-JUL-1997; 97US-008877.				
CC	probes which hybridise to GPCR polynucleotides and vectors	PR 03-JAN-2002; 2002US-0003959.				
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may	AX Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;				
CC	be used in the diagnosis, treatment or prevention of a wide variety of	XX				
CC	diseases including neurological disorders (e.g., Alzheimer's disease,	PN (WANG/) WANG W,				
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);	PA (GISH/) GISH K. C.				
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	PA (SCHA/) SCHALL T. J.				
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	PA (VICA/) VICARI A.				
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	PA (ZLOT/) ZLOTNIK A.				
CC	from the transgenic mice; kits comprising several mice, each of which has	XX				
CC	a mutation in a different GPCR gene of the invention; and kits comprising	PA (DCCR/) DENDRITIC CELL RECEPTOR				
CC	probes which hybridise to GPCR polynucleotides and vectors	XX				
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may	XX				
CC	be used in the diagnosis, treatment or prevention of a wide variety of	XX				
CC	diseases including neurological disorders (e.g., Alzheimer's disease,	XX				
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);	XX				
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	XX				
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	XX				
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	XX				
CC	from the transgenic mice; kits comprising several mice, each of which has	XX				
CC	a mutation in a different GPCR gene of the invention; and kits comprising	XX				
CC	probes which hybridise to GPCR polynucleotides and vectors	XX				
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may	XX				
CC	be used in the diagnosis, treatment or prevention of a wide variety of	XX				
CC	diseases including neurological disorders (e.g., Alzheimer's disease,	XX				
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);	XX				
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	XX				
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	XX				
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	XX				
CC	from the transgenic mice; kits comprising several mice, each of which has	XX				
CC	a mutation in a different GPCR gene of the invention; and kits comprising	XX				
CC	probes which hybridise to GPCR polynucleotides and vectors	XX				
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may	XX				
CC	be used in the diagnosis, treatment or prevention of a wide variety of	XX				
CC	diseases including neurological disorders (e.g., Alzheimer's disease,	XX				
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);	XX				
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	XX				
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	XX				
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	XX				
CC	from the transgenic mice; kits comprising several mice, each of which has	XX				
CC	a mutation in a different GPCR gene of the invention; and kits comprising	XX				
CC	probes which hybridise to GPCR polynucleotides and vectors	XX				
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may	XX				
CC	be used in the diagnosis, treatment or prevention of a wide variety of	XX				
CC	diseases including neurological disorders (e.g., Alzheimer's disease,	XX				
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);	XX				
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	XX				
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	XX				
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	XX				
CC	from the transgenic mice; kits comprising several mice, each of which has	XX				
CC	a mutation in a different GPCR gene of the invention; and kits comprising	XX				
CC	probes which hybridise to GPCR polynucleotides and vectors	XX				
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may	XX				
CC	be used in the diagnosis, treatment or prevention of a wide variety of	XX				
CC	diseases including neurological disorders (e.g., Alzheimer's disease,	XX				
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);	XX				
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	XX				
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	XX				
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	XX				
CC	from the transgenic mice; kits comprising several mice, each of which has	XX				
CC	a mutation in a different GPCR gene of the invention; and kits comprising	XX				
CC	probes which hybridise to GPCR polynucleotides and vectors	XX				
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may	XX				
CC	be used in the diagnosis, treatment or prevention of a wide variety of	XX				
CC	diseases including neurological disorders (e.g., Alzheimer's disease,	XX				
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);	XX				
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	XX				
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	XX				
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	XX				
CC	from the transgenic mice; kits comprising several mice, each of which has	XX				
CC	a mutation in a different GPCR gene of the invention; and kits comprising	XX				
CC	probes which hybridise to GPCR polynucleotides and vectors	XX				
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may	XX				
CC	be used in the diagnosis, treatment or prevention of a wide variety of	XX				
CC	diseases including neurological disorders (e.g., Alzheimer's disease,	XX				
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);	XX				
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	XX				
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	XX				
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	XX				
CC	from the transgenic mice; kits comprising several mice, each of which has	XX				
CC	a mutation in a different GPCR gene of the invention; and kits comprising	XX				
CC	probes which hybridise to GPCR polynucleotides and vectors	XX				
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may	XX				
CC	be used in the diagnosis, treatment or prevention of a wide variety of	XX				
CC	diseases including neurological disorders (e.g., Alzheimer's disease,	XX				
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);	XX				
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	XX				
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	XX				
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	XX				
CC	from the transgenic mice; kits comprising several mice, each of which has	XX				
CC	a mutation in a different GPCR gene of the invention; and kits comprising	XX				
CC	probes which hybridise to GPCR polynucleotides and vectors	XX				
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may	XX				
CC	be used in the diagnosis, treatment or prevention of a wide variety of	XX				
CC	diseases including neurological disorders (e.g., Alzheimer's disease,	XX				
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);	XX				
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	XX				
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	XX				
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	XX				
CC	from the transgenic mice; kits comprising several mice, each of which has	XX				
CC	a mutation in a different GPCR gene of the invention; and kits comprising	XX				
CC	probes which hybridise to GPCR polynucleotides and vectors	XX				
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may	XX				
CC	be used in the diagnosis, treatment or prevention of a wide variety of	XX				
CC	diseases including neurological disorders (e.g., Alzheimer's disease,	XX				
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);	XX				
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic	XX				
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a	XX				
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived	XX				
CC	from the transgenic mice; kits comprising several mice, each of which has	XX				
CC	a mutation in a different GPCR gene of the invention; and kits comprising	XX				
CC	probes which hybridise to G					

CC chemokine receptor showing sequence similarity to M/DCCR.

XX Sequence 374 AA;

SQ Query Match 100.0%; Score 1970; DB 8; Length 374;

Best Local Similarity 100.0%; Pred. No. 5.1e-215;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSPFRTNTNESEGETTTPDYDGPCKEDVKQIGAQQLPPLYSLVP1PGFVGN 60

Db 1 MLSTRSRSPFRTNTNESEGETTTPDYDGPCKEDVKQIGAQQLPPLYSLVP1PGFVGN 60

Qy 61 MLVVLILINGKRLKCLTDYLTLNLAISDLFLITLPLWAHSAANEWFGRNAMCKLFGTLY 120

Db 61 MLVVLILINGKRLKCLTDYLTLNLAISDLFLITLPLWAHSAANEWFGRNAMCKLFGTLY 120

Qy 121 HIGYGGIFTPLTIDRYLAIVAVFAFLKARTTYFGVWTSVITWLVAVASVPGIIFTK 180

Db 121 HIGYGGIFTPLTIDRYLAIVAVFAFLKARTTYFGVWTSVITWLVAVASVPGIIFTK 180

Qy 181 CQEDSVTYCPIPFRGWNFHITMNRNLGLVPLIMIVCYSGILKTLLRCNEKCHR 240

Db 181 CQEDSVTYCPIPFRGWNFHITMNRNLGLVPLIMIVCYSGILKTLLRCNEKCHR 240

Qy 241 AYRIFTIMIVYFLFWTPNIVLINTFOFGLSNCTESTSOLIDATOVTETLGTMTHCCI 300

Db 241 AYRIFTIMIVYFLFWTPNIVLINTFOFGLSNCBTSISQLDQATOVTETLGTMTHCCI 300

Qy 301 NPIYAFVGEKFRSLFHIAIGCRATAPLKQPVCGSPGVRSRGKVNVTQGLDGRGKGS1 360

Db 301 NPIYAFVGEKFRSLFHIAIGCRATAPLKQPVCGSPGVRSRGKVNVTQGLDGRGKGS1 360

Qy 361 GRAPEASLOKEGA 374

Db 361 GRAPEASLOKEGA 374

Qy 19-NOV-2002 (first entry)

Db 19-NOV-2002 (first entry)

Qy Class I receptors WSXWS motif.

Db Immunoglobulin; variable heavy chain; variable light chain; human;

Qy G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;

Db immunologic deficiency syndrome; blood protein disorder; nephritis;

Qy ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;

Db histiocytosis; chemotaxis; infectious disease; autoimmune disease;

Qy Addison's disease; dermatitis; rheumatoid arthritis; allergy;

Db neurodegenerative disorder; viral infection; poxvirus infection; HIV;

Qy human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;

Db pneumocytosis carni infection; cardiovascular disorder; atherosclerosis;

Qy lymphocytopenia.

Db Synthetic.

Qy OS.

Db WO200264612-A2.

Qy 22-AUG-2002.

Db PD 08-FEB-2002; 2002WO-US003634.

Qy XX PR 09-FEB-2001; 2001US-00779880.

PR 09-FEB-2001; 2001WO-US004153.

PR 12-JUN-2001; 2001US-0297257P.

PR 08-AUG-2001; 2001US-0310458P.

PR 12-OCT-2001; 2001US-0328447P.

PR 21-DEC-2001; 2001US-0341725P.

XX

Qy PD 08-AUG-2003 (first entry)

PA (HUMA-) HUMAN GENOME SCI INC.

XX PA XX

PI PI XX

DR DR XX

PT PT

PT PT

PT PT

XX XX

PS Example 17; Page 386; 562pp; English.

XX XX

CC The invention describes an isolated polynucleotide encoding a first

CC antibody at least 95-100% identical to a second antibody consisting of an

CC amino acid sequence comprising at least one, two or three CDR regions of

CC a variable heavy (VH) or variable light (VL) domain of the antibody

CC expressed by a hybridoma cell line consisting of XF3.5 F1, XF11.1F8,

CC XF3.6A2, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.43B5,

CC XF27/28.25G10, XF27/28.36A12, XF27/28.43B2. The antibody

CC is useful treating, preventing, ameliorating, ameliorating, prognosing or monitoring

CC cancers or other diseases or disorders e.g. immunologic deficiency

CC syndromes such as blood protein disorders and ataxia telangiectasia,

CC inflammation associated disorders such as endotoxin lethality, nephritis

CC and inflammatory bowel disease, conditions associated with an increase in

CC certain haemopoietic cells such as histiocytes, defective or aberrant

CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,

CC an infectious disease, an autoimmune disease such as Addison's disease,

CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative

CC disorder, a viral infection e.g. HRV infection, cytomegalovirus or

CC poxvirus infection, a pneumocytosis carni infection, Kaposi's sarcoma,

CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a

CC disease or disorder associated with aberrant expression of novel human G-

CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid

CC sequence of the WSXWS motif found in class I receptors

SQ Sequence 344 AA;

XX SQ

Qy Query Match 9

DB Best Local Similarity 92.5%; Score 1623; DB 5; Length 344;

Match 18; Pred. No. 2.5e-198;

Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 BEVTTFDFDYGAPCKEDVKQIGAQQLPPLYSLVIFP1FGVGM1LVVLLINCKLKCUT 77

Db 1 EEVTTFDFDYGAPCKEDVKQIGAQQLPPLYSIVFGFVGML1LVVLLINCKLKCUT 60

Qy 78 DIVVLLAISDLFLITPLWHAISANEWFGNAMCKLUTPLWHAISANEWFGNAMCKLUT 137

Db 61 DIVVLLAISDLFLITPLWHAISANEWFGNAMCKLUTPLWHAISANEWFGNAMCKLUT 120

Qy 138 RYLAIVHAVFALKARTTGFVWTSVITWLVAVASVPGIIFTKQKEDDSVYVCPYFPRG 197

Db 121 RYLAIVHAVFALKARTTGFVWTSVITWLVAVASVPGIIFTKQKEDDSVYVCPYFPRG 180

Qy 198 WNFHTIMVNLGLVPLIMIVCYSGIKLTKLRCNEKGRHRAVVFPTIMIVYFLFT 257

Db 181 WNFHTIMVNLGLVPLIMIVCYSGIKLTKLRCNEKGRHRAVVFPTIMIVYFLFT 240

Qy 258 PYNTVILANTFOFFGSLNCESTSQLDQATQVETLGNTHCCINPIITAFGKFRSFIFH 317

Db 241 PYNTVILANTFOBFGLNCESTSQLDQATQVETLGNTHCCINPIITAFGKFRSLFH 300

Qy 318 TALGCRIAPILOKPVCGGPGVRPGKVNKVTTQGLDGRGKGKSTG 361

Db 301 TALGCRIAPILOKPVCGGPGVRPGKVNKVTTQGLDGRGKGKSTG 344

RESULT 10

ABU61655

ID ID

ABU61655 standard; protein; 344 AA.

AC AC

ABU61655;

XX XX

DT 08-AUG-2003

activity and can be used for gene therapy. The G-protein chemokine receptors, HDGNR10, (I) are useful for screening for compounds which activate or inhibit activation of (I). The products of the invention can also be used for stimulating haemopoiesis, wound healing, coagulation, angiogenesis, treating solid tumours, chronic infections, leukemia, T-cell mediated autoimmune diseases, parasitic infections, psoriasis, and stimulating growth factor activity. HDGNR10 is useful for treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin B (IgB)-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-sinophilic syndrome. (N.B. This record was resubmitted to correct errors in the keyword formatting)

Sequence 329 AA:

Query	87.7%; Score 1727.5; DB 4;	Length 329;	PI Li Y., Ruben SM;
Best Local Similarity	95.6%; Pred. No. 1.8e-187;	DB 5;	XX WPI; 2002-598724/64.
Matches	329; Conservative 0; Mismatches 0;	Gaps 1;	XX New polynucleotide encoding a human G protein chemokine receptor HDGNR10, useful e.g. for treating tumors.
Db	1 EEEVTFDDYDYGAPCKHEPDVKQGAQQLPPLYSLVEFGGVNMMLVVYLILINCKKLKCLT 60	XX Example: Fig 2; 22pp; English.	XX
Qy	78 DIVYLNLAISDLFLITLPLWAISAAANEWFGNAMCKLFTGLYHIGYFGGIFPILLID 137	XX	The invention relates to a novel human 7-transmembrane receptor, HDGNR10, which has been identified as a G-protein chemokine receptor. The GPCR HDGNR10 polypeptide can be expressed by standard recombinant methodology. Compounds that activate or inhibit the receptor polypeptide, optimally expressed from DNA in gene therapy vectors, are used to treat diseases that require: (a) activation of the receptor (e.g. stimulation of haemopoiesis, treatment of solid tumours, T-cell mediated autoimmune diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis etc.). The present sequence represents human MCP-1 receptor used in comparison studies with the HDGNR10 receptor
Db	61 DIVYLNLAISDLFLITLPLWAISAAANEWFGNAMCKLFTGLYH----- 105	XX	XX
Qy	138 RYLAIVHAFALKARTVTFGVTTSVITLVAFAVSPGIIIFTIKCQEDSVVYCGPYPPRG 197	XX	XX
Db	106 RYLAIVHAFALKARTVTFGVTTSVITLVAFAVSPGIIIFTIKCQEDSVVYCGPYPPRG 165	XX	XX
Qy	198 WNNFHMTMRNLIQGYPLIIMVYPLFWT 257	XX	XX
Db	166 WNNFHMTMRNLIQGYPLIIMVYPLFWT 225	XX	XX
Qy	258 PYNTVILANTFOEFFGLSNCESTSSQLDQATQTEFLGTHCCINPIIYAFGEKERSLFH 317	XX	XX
Db	226 PYNTVILANTFOEFFGLSNCESTSSQLDQATQTEFLGTHCCINPIIYAFGEKERSLFH 285	XX	XX
Qy	318 IALGCRIAPLQKEVCGGSGVRPGKVNKVTTQJLDGRKGKSTG 361	XX	XX
Db	286 IALGCRIAPLQKEVCGGSGVRPGKVNKVTTQJLDGRKGKSTG 329	XX	XX
RESULT 14		XX	XX
ABB81055	ID ADR16266 standard; protein; 329 AA.	XX	XX
XX	AC ADR16266;	XX	XX
XX	DT 05-NOV-2002 (first entry)	XX	XX
DE Human MCP-1 receptor.	ID ADR16266 standard; protein; 329 AA.	AC ADR16266;	XX
XX	KW 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10;	XX	XX
KW G-protein chemokine receptor; hematopoietic; immunosuppressant;	KW antiparasitic; anti-psoriatic; anti-allergic; anti-inflammatory; cyrostatic;	AC DT 21-OCT-2004 (first entry)	XX
KW anti-neumatic; antiarthritic; gene therapy; human; MCP-1; receptor.	KW Homo sapiens.	DE Human MCP-1 receptor fragment.	XX
OS Homo sapiens.	PN US2002076745-A1.	DE G-protein chemokine receptor; CCR5; HDGNR10; allergy; atherogenesis;	XX
XX	PA (LIYY/) LI Y.	KW anaphylaxis; malignancy; inflammation; prostatitis; atherosclerosis;	XX
PA (RUBE/) RUBEN S M.	PA	KW bone marrow failure; silicosis; sarcoidosis; rheumatoid arthritis; shock;	XX
XX	XX	KW hyperesinophilic syndrome; haematopoiesis; wound healing; coagulation;	XX
PR 06-JUN-1995;	PR 95US-00466343.	KW angiogenesis; solid tumour; chronic infection; leukaemia;	XX
XX	PR US2004151719-A1.	KW autoimmune disease; parasite; parasitic infection; psoriasis; human;	XX
XX	XX	KW Homo sapiens.	OS
XX	XX	XX	PN US2004151719-A1.

new isolated antibody that binds to an extracellular portion of human G-

Protein chemokine receptor 5 (CCR5) (also known as **HDGNR10**), useful for treating conditions such as allergies, cancers, and inflammation.

disclosure; SEQ ID NO 9; 23pp; English.

The invention provides a human G-protein chemokine receptor (CCB5) homologous to HDGNR10 polynucleotide, polypeptides, and antibodies. The antibody that is an antagonist of HDGNR10 is potentially useful for preventing or treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE-mediated allergic reactions, sarcoidosis, rheumatoid arthritis, shock and hypereosinophilic syndrome, the compounds that bind to and activate the receptor are potentially useful for stimulating haemopoiesis, wound healing, coagulation and angiogenesis, and in treating solid tumours, chronic infections, leukaemia, T-cell mediated auto-immune diseases, parasitic infections and vasculitis. The antibody may also be used as a diagnostic reagent. The present sequence is a human MCP-1 receptor fragment (residues 18-361) which shares homology with the G-protein chemokine receptor (CCRS5) (residues 1-361 of the human MCP-1 receptor).

卷之三

3Q Sequence 329 AA;

Query Match Score 1727.5; DB 8; Length 329;
 Best Local Similarity 95.6%; Pred. No. 1; e=187;

1 EETTTFDYGAPCHKFDVKIQGAQLPPLYSLWTFGTGNMLVLLINCKLKCFL 60

78 DIVLNIAISDLPLITLWAHSAAANEVFGNAMCKLFTGGLYHIGYFGGIFPIILITID 13

61 DYLINLAISDLLFLITPLWAHSRAANEWVGNAMCQLFTGLYHI
62 DYLINLAISDLLFLITPLWAHSRAANEWVGNAMCQLFTGLYHI

Yy	138	RYLAIVHAFALKARTVFGVVTSITWLVAYFASVPGIIFTKQKEISVYVGPyPRG
bb	106	RYLAIVHAFALKARTVFGWTTSITWLVAYFASVPGIIFTKQKEISVYVGPyPRG

198 WNNFTIMRNLIGLYPLMLIVCYSGLKILKTLLRCNECCRRAVRYIFTIMIVFPLFWT 254

166 WNNFTITMRNLLGIVPLPLIMVICYSGLIKTTLRCRNECKRRAVRYIFTIMIVTEFWT 225

258	PYNTVILINTFOEPFGNSCRSTQDQATOVTBLGMTHCCINPPIIAFGVKRFLPH	311
226	PYNTVILINTFOEPFGNSCRSTQDQATOVTBLGMTHCCINPPIIAFGVKRFLPH	286

318 IALGCRIAPIPLQKPVCGGPVPGPKVTTGQLIDGRGKGKSG 361
320

286 IALGCRRIAPLQKPVCGGPGR.PGKNVKVTTQGLLDGRGKGSIG 329

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Qy	241	AVRVIFTIMIVYVLEFWTPNIVILNTPQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300	Qy	241	AVRVIFTIMIVYVLEFWTPNIVILNTPQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300		
Db	241	AVRVIFTIMIVYVLEFWTPNIVILNTPQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300	Db	241	AVRVIFTIMIVYVLEFWTPNIVILNTPQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300		
Qy	301	NPIIYAFGEKFRSLFHTALGCRITAPLQRPVCGSPGVPGKVNVTQGLDGRGKGS1	360	Qy	301	NPIIYAFGEKFRSLFHTALGCRITAPLQRPVCGSPGVPGKVNVTQGLDGRGKGS1	327		
Db	301	NPIIYAFGEKFRSLFHTALGCRITAPLQRPVCGSPGVPGKVNVTQGLDGRGKGS1	360	Db	301	NPIIYAFGEKFRRLSVFFRKHITKPFCKQCFCV	334		
Qy	361	GRAPEASLQDKEGA	374	Db	361	GRAPEASLQDKEGA	374		
RESULT 3									
		A43113							
		chemokine (C-C) receptor 5 - human							
		N;Alternate names: C-C CKR-5; CCRS							
		C;Species: Homo sapiens (man)							
		C;Accession: A43113; 871808; A58834; A58832; G02653; A58633							
		C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004							
		C;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor							
		A;Reference number: A43113; MUID:8639485							
		A;Accession: A43113							
		A;Molecule type: mRNA							
		A;Residues: 1-352 <S4M1>							
		A;Cross-references: GB:X91492; NID:91262810; PIDN:CA62796.1; PID:91262811							
		P;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Parber, C.M.; Saragosti, M.; Imai, T.; Rana, S.; Xi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa							
		Nature 338, 722-725, 1996							
		A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of							
		A;Reference number: S71808; MUID:875144							
		A;Accession: S71808							
		A;Status: nucleic acid sequence not shown; not compared with conceptual translation							
		A;Molecule type: DNA							
		A;Residues: 182-206; 207-230 <S4M2>							
		A;Accession: A58834							
		A;Status: nucleic acid sequence not shown; not compared with conceptual translation							
		A;Molecule type: DNA							
		A;Residues: 1-184, 'IKDSHLGAGPAACGHILLGPKNASVSK' <S4M3>							
		A;Cross-references: GB:X9993; NID:91524062; PIDN:CA67767.1; PID:91524063							
		A;Note: this frameshift mutation results in a non-functional receptor but confers a degree							
		nd may have had a selective advantage by conferring resistance to Yersinia plague infecti							
		R;Combidere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.							
		C;Superfamily: vertebrate rhodopsin							
		C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran							
		F;43-70/Domain: transmembrane #status predicted <TM1>							
		F;81-100/Domain: transmembrane #status predicted <TM2>							
		F;115-136/Domain: transmembrane #status predicted <TM3>							
		F;154-178/Domain: transmembrane #status predicted <TM4>							
		F;207-226/Domain: transmembrane #status predicted <TM5>							
		F;244-268/Domain: transmembrane #status predicted <TM6>							
		F;287-319/Domain: transmembrane #status predicted <TM7>							
		F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted							
		F;113-190/Disulfide bonds: #status predicted							
Query Match	83.8%	Score 1651.5; DB 2; Length 360;							
Best Local Similarity	95.5%	Pred No. 7.1e-137;							
Matches	319;	Conservative	3;	Mismatches	5;	Indels	7;	Gaps	3;
Qy	1	MLSTSRSPRFRTNTNESGEVTTFDYDGAPCKFDVQIQAGQLPLPYSVIFGFVGN	60	Db	61	MLVFLILNCKLKCLTDYLNLIAISDLPLTLPLMAHSAAANEWFGNAMCKLFPGLY	120		
Db	1	MLSTSRSPRFRTNTNESGEVTTFDYDGAPCKFDVQIQAGQLPLPYSVIFGFVGN	60	Qy	121	HIGYFGGIPPFILLTIDRYLAIVHAVALKARTTVFGVTVSITWLVAAPASVPGIIFTK	180		
Qy	61	MLVFLILNCKLKCLTDYLNLIAISDLPLTLPLMAHSAAANEWFGNAMCKLFPGLY	120	Db	121	HIGYFGGIPPFILLTIDRYLAIVHAVALKARTTVFGVTVSITWLVAAPASVPGIIFTK	180		
Db	61	CQEDSVVYCGPFPGRMNFFTMRLTGLVPLLINVTCYSGILKTLRCNEKRRH	240	Qy	181	CQEDSVVYCGPFPGRMNFFTMRLTGLVPLLINVTCYSGILKTLRCNEKRRH	240		
Db	181	CQEDSVVYCGPFPGRMNFFTMRLTGLVPLLINVTCYSGILKTLRCNEKRRH	240	Db	181	CQEDSVVYCGPFPGRMNFFTMRLTGLVPLLINVTCYSGILKTLRCNEKRRH	240		

/Note: probably acts to control granulocyte proliferation and differentiation
 /Superfamily: vertebrate rhodopsin
 /Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM1>
 /32-56/Domain: transmembrane #status predicted <TM2>
 /67-87/Domain: transmembrane #status predicted <TM2>
 /103-124/Domain: transmembrane #status predicted <TM3>
 /142-166/Domain: transmembrane #status predicted <TM4>
 /193-218/Domain: transmembrane #status Predicted <TM5>
 /236-257/Domain: transmembrane #status Predicted <TM6>
 /285-300/Domain: transmembrane #status Predicted <TM7>
 /20-269,101-178/disulfide bonds: #status predicted
 /268,337,342/Binding site: carbohydrate (Asn) (covalent) #status predicted
 /336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
 /340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match	Score	DB	Length
Best Local Similarity	62.1%	Score 1224;	DB 2;
Pred. No.	76.3%	Length 352;	
Matches	235;	No. 1-8e-99;	
Matches	235;	Mismatches 34;	
		Indels 12;	Gaps 3;
by			
24	FDYD--GAPCHKFVDYQIGAQOLLPLPPLSVPFIGFVGNMVLVLLINCKKLKCITDYL	81	
10	YDINYTTSBPQKINVQIAARLPLPPLSFLVFIGVGNMVLVLLINCKRLKSLTIDYL	69	
by			
82	LNAISDLLEFLITLPWAHSAAANEVNGNAMCKLFLGVLHIGYFGGIFFFLILLTIDRYLA	141	
70	LNLATESDLLEFLITLPWAHZAAAONDGFNTMCQULLTGGLPFIGFGGIFFFLILLTIDRYLA	129	
by			
142	IHAVEFALKARTVTFGVTSVITWVAVFAVSPGIIPTFCQKEDSVVYCGPYFP-----RG	197	
130	VHAVEFALKARTVTFGVTSVITWVAVFASLPGIIFTTSQKEGHYTSSSHPFYSQQF	189	
by			
198	WNNFHTTMNRTLIGLYVLPILLIMIVCYSGILKTLLRCNEKKHRRAVRVITIMITYFLFWT	257	
190	WRKNFQLKIVLGVLVPLVVVICYSGLKTLLRCNEKKHRRAVRVITIMIVYFLFWA	249	
by			
258	PYNIVLILANTFORFFGNSCBESTSQLDQAQTVETLGMTHCCINPIIYAFVGKEFRSLP-	316	
250	PYNIVLILANTQEFFGLNNCSSSNRQLDQANQTVETLGMTHCCINPIIYAFVGKEFRNTYL	309	
by			
317	----HIA	319	
310	WPEOCH	317	

PAGINA 4

hemokine (C-C) receptor 1 - human
;Alternate names: C-C CRK-1; macrophage inflammatory protein-1-alpha receptor
;Species: Homo sapiens (man)
;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
;Accession: A45177; IS5671
;Note: K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
;ell 72 415-425, 1993
;Title: Molecular cloning, functional expression, and signaling characteristics of
;Reference number: A45177; MUID:3161416; PMID:7679328
;Accession: A45177

:Molecule type: mRNA
:Residues: 1-355 <RBO>
:Cross-references: UNIPROT:P22246; GB:L10918; NID:g292416; PID:AAA36543.1; PID:
:Experimental source: HL60 cells
:Note: sequence extracted from NCBI backbone (NCBIP:124876)
:Gao, J.
:Exp. Med. 177, 1421-1427, 1993
:Title: Structure and functional expression of the human macrophage inflammatory
:Reference number: 155671; MUID:93240122; PMID:7683036
:Accession: 155671
:Status: preliminary
:Translated from GB/EMBL/DDBJ
:Molecule type: mRNA
:Residues: 1-355 <RBS>
:Cross-references: GB:L10918; NID:g292416; PID:AAA36543.1; PID:g292417
:Genetics:
:Gene: GDB:CMKBR1; CMKR-1

A; Cross-references: GDB:1138446; OMIM: 601159
 A; Map Position: 3p21-3p21
 C; Superfamily: vertebrate rhodopsin
 C; Keywords: disulfide bond; G protein-coupled
 F; 36-60/Domain: transmembrane #status predi
 F; 71-91/Domain: transmembrane #status predi
 F; 108-129/Domain: transmembrane #status predi
 F; 147-171/Domain: transmembrane #status predi
 F; 205-223/Domain: transmembrane #status predi
 F; 240-364/Domain: transmembrane #status predi
 F; 288-305/Domain: transmembrane #status predi
 F; 5/Binding site: carbohydrate (Asn) (coval)
 F; 24-273,106-183/Disulfide bonds: #status p
 F; 345/Binding site: phosphate (Ser) (coval)

Query Match	Score	967
Best Local Similarity	49.1%	
Matches 185; Conservative	58.7%	Pred. No.
Matches 47;	Mismat	
Qy	12	NTNESGBEVTFFDDYGA[PCHKFVDYKQI
Db	5	NTVTD-YDRTTEFDGDATCQKVNRNRAF
Qy	72	KLKCLTDIVLNLAISDLLEPLITLPLWA-1
Db	64	RKQMTSIVYLNLAAISDLLEPLTLPWID
Qy	131	ILLITIDRYLAIVHAEVALLARTVFGVV
Db	124	ILLITIDRYLAIVHAEVALLARTVFGVII
Qy	191	GPyFP---RGWNNFHTMINILGLVLPPL
Db	184	SLPHFESLRLWKLFOAQLNLFLGLVLPPL
Qy	247	TIMIVYPLFPTPYNIVLNLNTFQEFGGLSI
Db	243	VIMIFPLFPTPYNLTILISVFOQDPLFTHI
Qy	307	FVGKEP---RSLFH 3.17
Db	303	FVGPBPBPKVYBOLH 3.17

5 DECEMBER

I49341 MIP-1 alpha receptor like-2 - mouse
C;Species: *Mus musculus* (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-JL
C;Accession: I49341
R;Gao, J.L.; Murphy, P.M.
J.Biol.Chem. 270, 1794-17501, 1995
A;Title: Cloning and differential tissue-specific expression of the mouse MIP-1alpha receptor
A;Reference number: I49339; MUID: 95340546;
A;Accession: I49341
A;Status: preliminary; translated from GB/EBI

Qy	129	FPIILLTIDRYLAIYHAYPALKARTVTFGVVTSVITWLYAVFASVPGIIFTKQKEDSVY	188	C;Accession: G02436; A57237
Db	126	FPIILLTIDRYLAIYHAYPALKARTVTFGVVTSVITWLYAVFASVPGIIFTKQKEDSVY	185	Submitted to the EMBL Data Library, February 1996
Qy	189	VCGFYFPRG---WNNFHTIMRLNTIGLVPLLLIVMIVCYSGILTKLRCNEKEGRHRAVR	244	A;Reference number: H01272
Db	186	SCSPRYPEGEEDSWKRHALRNNIFGLALPILLYVIVCYSGILTKLRCPN-KGGHKAIRL	244	A;Status: translated from GB/EMBL/DBJ
Qy	245	IIFTMIVYPLFLTPNIVLNLNTQEPPFCISNCESTSOLDAQTVETLGFMTHCTINPLI	304	A;Molecule type: DNA
Db	245	IFVNIVIPFIFWTPNVLVLSAFHSTPLTECSQSKHDLAMQTVETIAVTHCCVNPVI	304	A;Cross-references: UNIPROT: P51677; EMBL: U49727; NID: g1477560; PID: g1477560; R;Combadiere, C.; Ahuij, S.K.; Murphy, P.M.
Qy	305	YAFGEKERS---LFHTAGCRTRAPLKQPVCGGPVTPRGKVKVYQGL--LDGRGKG	357	J. Biol. Chem. 270, 16491-16494, 1995
Db	305	YAFGEKERS---LFHTAGCRTRAPLKQPVCGGPVTPRGKVKVYQGL--LDGRGKG	341	A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
Qy	358	KSIGRAPEAQLDQ	370	A;Reference number: A57237; MUID: 95348056; PMID: 7622448
Db	342	RTSSVSPSTGQE	354	A;Status: nucleic acid sequence not shown
Qy	358	KSIGRAPEAQLDQ	370	A;Molecule type: mRNA
Db	342	RTSSVSPSTGQE	354	A;Cross-references: GB: U28694; NID: g1199579; PID: g1199580
Qy	358	KSIGRAPEAQLDQ	370	A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN: AAC50469.1
Db	342	RTSSVSPSTGQE	354	C;Genetics:
Qy	358	KSIGRAPEAQLDQ	370	A;Gene: GDB: CMKB3
Db	342	RTSSVSPSTGQE	354	A;Cross-references: GDB: 579624; OMIM: 601268
Qy	1433	I49339	macrophage inflammatory protein-1 alpha receptor - mouse	A;Map position: 3p21-3p21
Db	1433	I49339	C;Species: Mus musculus (house mouse)	C;Superfamily: vertebrate rhodopsin
Qy	1433	I49339	C;Accession: I49339	C;Keywords: G protein coupled receptor; Glycoprotein; phosphoprotein; transmembrane protein
Db	1433	I49339	R;Gao, J.L.; Murphy, P.M.	F: 16-60/Domain: transmembrane #status Predicted <TM>
Qy	1433	I49339	C;Accession: I49339	F: 71-91/Domain: transmembrane #status Predicted <TM2>
Db	1433	I49339	R;Gao, J.L.; Murphy, P.M.	F: 10-129/Domain: transmembrane #status Predicted <TM3>
Qy	1433	I49339	C;Accession: I49339	F: 147-171/Domain: transmembrane #status Predicted <TM4>
Db	1433	I49339	R;Gao, J.L.; Murphy, P.M.	F: 205-223/Domain: transmembrane #status Predicted <TM5>
Qy	1433	I49339	C;Accession: I49339	F: 240-261/Domain: transmembrane #status Predicted <TM6>
Db	1433	I49339	R;Gao, J.L.; Murphy, P.M.	F: 288-305/Domain: transmembrane #status Predicted <TM7>
Qy	1433	I49339	C;Accession: I49339	F: 24-273-106-183/Disulfide bonds: #status Predicted
Db	1433	I49339	R;Gao, J.L.; Murphy, P.M.	F: 345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status Predicted
Qy	1433	I49339	C;Cross-references: UNIPROT: P51675; EMBL: U28404; NID: g881547; PIDN: AAA89153.1; PID: g8815	Query Match Score 45.2t; Best Local Similarity 54.6t; Matches 167; Conservative 56; Mismatches 72; Indels 11; Gaps 5;
Db	1433	I49339	C;Superfamily: vertebrate rhodopsin	Query Match Score 890.5; DB 2; Best Local Similarity 54.6t; Matches 170; Conservative 58; Mismatches 56; Indels 11; Gaps 5;
Qy	21	TTEFDYDGAPCKHCPDKVQIGAQQLPPLYSVTPFGVNMMLVVLINCKKLKCTUDIY	80	21 TTEFDYDGAPCKHCPDKVQIGAQQLPPLYSVTPFGVNMMLVVLINCKKLKCTUDIY 80
Db	13	TTEFDYDGAPCKHCPDKVQIGAQQLPPLYSVTPFGVNMMLVVLINCKKLKCTUDIY	80	Db 14 TSYTD-DVGLLCEKADTRALMAQFVPPVPLSVTVGQVNVVMMIJKYRRRIMNNY 72
Qy	21	LLNLAISDLPLTLPLMAHSA-ANEWVFGNAMCKLFPTGLYHIGYFGGGIFPLLTIDRY	139	Qy 81 LLNLAISDLPLTLPLMAHSA-ANEWVFGNAMCKLFPTGLYHIGYFGGGIFPLLTIDRY 139
Db	13	LLNLAISDLPLTLPLMAHSA-ANEWVFGNAMCKLFPTGLYHIGYFGGGIFPLLTIDRY	139	Db 73 LLNLAISDLPLTLPLMAHSA-ANEWVFGNAMCKLFPTGLYHIGYFGGGIFPLLTIDRY 132
Qy	81	LLNLAISDLPLTLPLMAHSA-ANEWVFGNAMCKLFPTGLYHIGYFGGGIFPLLTIDRY	139	Qy 140 LAIYHAVALKARTVTFGVVTSVITWLYAVFASVPGIIFTKQKEDSVYVCPYFPR --- 196
Db	73	LLNLAISDLPLTLPLMAHSA-ANEWVFGNAMCKLFPTGLYHIGYFGGGIFPLLTIDRY	132	Db 133 LAIYHAVALKARTVTFGVVTSVITWLYAVFASVPGIIFTKQKEDSVYVCPYFPR --- 192
Qy	140	LAIYHAVALKARTVTFGVVTSVITWLYAVFASVPGIIFTKQKEDSVYVCPYFPR ---	195	Qy 197 -GNNNFITIMRLIGLVPLLLIVCYSGLTLLRCNEKEGRHRAVRVFTIMIVPLF 255
Db	133	LAIYHAVALKARTVTFGVVTSVITWLYAVFASVPGIIFTKQKEDSVYVCPYFPR ---	192	Db 193 YSPRNHFITMLIGLVPLLLIVCYSGLTLLRCNEKEGRHRAVRVFTIMIVPLF 251
Qy	196	RGMNNFEHTIMRLNTIGLVPLFLTPNIVLNLNTQEPPFCISNCESTSOLDAQTVETLGFMTHCTINPLI	255	Qy 256 WTPYNVILVILNTQEPFOLSNCESTSOLODAQTVETLGFMTHCTINPLIAYFGEKRS- 314
Db	193	KONFRFOAHLTRPLVLLQPLVLMVTCYACITRILR-RPESEKVKAVRLFAITLLPFL	251	Db 252 WTPYNVILVILNTQEPFOLSNCESTSOLODAQTVETLGFMTHCTINPLIAYFGEKRS- 314
Qy	256	WTPYNVILVILNTQEPFOLSNCESTSOLODAQTVETLGFMTHCTINPLIAYFGEKRS-	312	Qy 315 ---LHF 317
Db	252	WTPYNLSEVSAFQDVLFTNQCESOKHDLAMQTVETIAVTHCCVNPVIIYFGERFWKY	311	Db 312 LRHFFH 317
Qy	313	-RSLF--HIALGERTRAPLK	329	RESULT 8
Db	312	LRQLFQRHVAI-----PLAK	326	JC4587
Qy	313	-RSLF--HIALGERTRAPLK	329	chemokine (C-C) receptor 4 - mouse
Db	312	LRQLFQRHVAI-----PLAK	326	C;Species: Mus musculus (house mouse)
Qy	313	-RSLF--HIALGERTRAPLK	329	C;Accession: JC4587
Db	312	LRQLFQRHVAI-----PLAK	326	R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Qy	313	-RSLF--HIALGERTRAPLK	329	Biochem. Biophys. Res. Commun. 218, 337-343, 1996
Db	312	LRQLFQRHVAI-----PLAK	326	C;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
Qy	313	-RSLF--HIALGERTRAPLK	329	C;Date: 21-Dec-1995 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

RESULT 7
G02436
Chemokine (C-C) receptor 3 - human
N;Altname: C-C CKR-3
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1995 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

RESULT 7
G02436
Chemokine (C-C) receptor 3 - human
N;Altname: C-C CKR-3
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1995 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

A;Reference number: JC4587; MUID:96136324; PMID:8573157
A;Accession: JC4587
A;Molecule type: mANA
A;Residues: 1-360 <HOO>
A;Cross-references: UNIPROT:P51680; EMBL:X90862; NID:91167851; PID:CAA62372.1; PID:g116
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; receptor; thymus
P;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
P;72,202,250/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
P;145,151/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
P;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 42.2%; Score 831.5%; DB: 2; Length 360;
Best Local Similarity 51.9%; Pred. No. 3.0e-65;
Matches 154; Conservative 58; Mismatches 80; Indels 5; Gaps 3;

Qy 31 PCKHFDVKOIGAQQLPLPLSIVFPGYGNMLVYLILNCKLKCLTDIYLNLALASDIL 90
Db 28 PCTKEGIAFKAFGLFLPPLPLSIVFPGYGNLSVYLVLPKRYKLRSMTDVYLNLALASDIL 87

Query Match 42.3%; Score 833.; DB 2; Length 360;
Best Local Similarity 47.9%; Pred. No. 2.9e-65;
Matches 160; Conservative 63; Mismatches 89; Indels 22; Gaps 5;

Qy 10 IRTNTNESGEVTFFDYD-YGAPCHKFEDYDVKOIGAQQLPLPLSIVFPGYGNMLVYLIL 68
Db 6 VTDTPQDETYNSYYFESNPCKPCPRGIKAFGEVFLPPLPLSIVFPGYGNMLVYLIL 65

Qy 69 NCKKLKCLTDIYLNLALASDILFLITLPLWAHSAAANEVNGNAMCKLFLGQHGYFGGI 128
Db 66 KYKRKLSMTDVYLNLALASDILFLPSLPPGYYAADDQVYGLGLCKTVSWMLVQGVFSI 125

Qy 129 FFIITLTIDYLAIATHAVFLKARTVTFPGVTTSTVTLVAVFASVPGIITPKCOKEDSVY 188
Db 126 PFIMLMSIDYLAIATHAVSLKARTLTGVTSLTIVSVAFLSPLGFLISTCYTERAHNT 185

Qy 189 VCGPYF---PRGMNNFHFTMRNLTGVLPLIMIVCYSSILKTLLRCRNKBRKHRAVRYI 245
Db 186 YCKTQSYNSNTTWKVLSLITNVLGGLPQGIMFLWYSNIIRTLOHQCNNEKK-NRAVMI 244

Qy 246 PTIMIVYFLWTPIVILLANTPQQFGGNSNCTESTSOLQDQATQVTEIGMTHCCINPITY 305
Db 245 FGVVVLFELGWTPTVNVFLFETLYLEVLDCTLERYDAIQATELTGFHCCINPITY 304

Qy 306 AFVGEKFR---SUFHIALGCRIALPQKEPVCGGP 335
Db 305 FFLGEKFRKXITQLFR-----TCRGF 325

RESULT 9
A57160
N;Alternate names: C-C receptor 4 - human
C;Species: Homo sapiens (man)
C;Accession: A57160
R;Power, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor c
A;Reference number: A57160; MUID:95370289; PMID:7642634
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: UNIPROT:P51679; GB:X85740; NID:91370103; PID:CAA59743.1; PID:g97145
A;Note: source clone KS-5
C;Genetics:
A;Gene: GDB:CKKBR4
A;Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
P;40-65/Domain: transmembrane #status predicted <TM1>
P;76-97/Domain: transmembrane #status predicted <TM2>
P;112-133/Domain: transmembrane #status predicted <TM3>
P;151-175/Domain: transmembrane #status predicted <TM4>
P;218-228/Domain: transmembrane #status predicted <TM5>
P;243-264/Domain: transmembrane #status predicted <TM6>

Query Match 40.3%; Score 794.5%; DB 2; Length 383;
Best Local Similarity 44.3%; Pred. No. 7.2e-62;
Matches 164; Conservative 60; Mismatches 107; Indels 39; Gaps 7;

Qy 4 TSSRFRFIRNTNESEGGVTFEDYD---GAPCHKFEDVKQIGAQQLPLPLSIVFPGVGNM 61
Db 32 TTAISLVSPTNSSEDYDDDDVYEEASAPCYKSDTTRIAQVPAVLLVLEFLGLGNI 91

Query Match 40.3%; Score 794.5%; DB 2; Length 383;
Best Local Similarity 44.3%; Pred. No. 7.2e-62;
Matches 164; Conservative 60; Mismatches 107; Indels 39; Gaps 7;

Qy 62 LIVYLILNCKLKCLTDIYLNLALASDILFLITLPLWAH--SAANEVYFGNAMCKLFLGTL 119
Db 92 LVIYIVTRYMKIKLNLNLALASDILFLITLPLWVHHYIGMYHDWTFGISMOKLKGNI 151

Query Match 40.3%; Score 794.5%; DB 2; Length 383;
Best Local Similarity 44.3%; Pred. No. 7.2e-62;
Matches 164; Conservative 60; Mismatches 107; Indels 39; Gaps 7;

Qy 120 YHGYFGGIPPFILLTITDYLAIATHAVFLKARTVTFPGVTSVITWLWAVFAVSYPGIFT 179
Db 152 CYMSLSSQVCFCILLTDYRLAVVAYTALRFRFTVTCGIVCTWFLAGLSLPEFPFH 211

Query Match 40.3%; Score 794.5%; DB 2; Length 383;
Best Local Similarity 44.3%; Pred. No. 7.2e-62;
Matches 164; Conservative 60; Mismatches 107; Indels 39; Gaps 7;

Qy 180 KCOKEDSYVCGPYFP---RGHNNFHFTMRNLTGVLPLIMIVCYSSILKTLLRCRNE 235
Db 212 GHQDDNNGRVQCDPYPMSNTVRRAYAKVIMSLIPLIIMAVCVRVIIIRLL-RPS 270

Query Match 40.3%; Score 794.5%; DB 2; Length 383;
Best Local Similarity 44.3%; Pred. No. 7.2e-62;
Matches 164; Conservative 60; Mismatches 107; Indels 39; Gaps 7;

Qy 236 KKHRRAVRFIFTIMIVYFLWTPTVNVILLNTFOEPFGUSNCESTSOLQATQVTEITGM 295
Db 271 KCCYKAIRLIFIMVAVFVWTPVNVILLSTTHATLNQCALSSNDMALITKTVAY 330

Qy 296 THCCINPIIYAFVGEKFR---SLFHIALG---CRIAPLQKPVCGGPGRPGKAVKVTTQ 348
 Db 331 THCCINPIIYAFVGEKFRHLVHFHTTVAVIYLCKYIP----- 368

Qy 349 GLUDGRGKCK 358
 Db 369 -FLSGDGBCK 377

RESULT 11

I49340 MTP-1 alpha receptor like-1 - mouse
 C:Accession: I49340
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 R:Gao, J. L.; Murphy, P.M.
 J. Biol. Chem. 270: 17494-17501, 1995
 Article: Cloning and differential tissue-specific expression of three mouse beta chemokine
 A:Reference: 149339; MUID:95340546; PMID:7542241
 A:Accession: I49340
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Residues: 1-356 <RES>
 A:Cross-references: UNIPROT:P51676; EMBL:U28405; NID:9881549; PIDN:AAA89154.1; PID:98815
 C:Superfamily: vertebrate rhodopain

Query Match 36.7%; Score 723; DB 2; Length 355;
 Best Local Similarity 43.5%; Pred. No. 1.e-55;
 Matches 131; Conservative 59; Mismatches 103; Indels 8; Gaps 3;

Matches 137; Conservative 59; Mismatches 92; Indels 6; Gaps 3;

Qy 25 DYDGAPCHKFVDQIGAQOLPPPLYSVIFGFPGVGNMLUVLLILNCKLQLCTDIYLN 84
 Db 18 DMSGFLCPSPINVRAFGITVPTPLSYVPIIGVIGHVLWVLIQHRLRLRNTSIVLFNL 77

Qy 85 AISDLFLITLPLWA-HSRANNEWVFGNAMCKLFTGLYHIGYFGGIFFILLTIDRYLAIV 143
 Db 78 AISDLVLSTLPFWVVDYIMKGDWLFGNAMCKFVSGFYTLGLYSDMFFLTLLTDRLAIV 137

Qy 144 HAYPAALKARTTYTGSVTSVITLVAEASVPG31IFTKQKEDSVVVGPFYFR---GWN 199
 Db 138 HVPFLARAKTVTGFISSITWLAALYSVCLXVFQSMEFYHTCRAILPRKSLLIRFL 197

Qy 200 NFHTIMRNILGLVPLLMICVYCSGILKTLRCRNEKRRRAVVFIMIVYPLFWTPY 259
 Db 198 RFQLTMTNIGLILPILLAMICVYTRIINVLHR-RPNKKAKAVKRLIFVITLFFLILAPY 256

Qy 260 NIVILLNTFOBFFGLNSCESTSOLQATOVTETLGTMTHCCINPIIYAFVGKFR 313
 Db 257 YLAFAVSAPDFVLEPLTPSCURSQQVDLSLMIATELAYTCVNPVIYVFVGKFR 310

Qy 313 R 313
 Db 308 K 308

RESULT 12

JCS067 G protein-coupled receptor CKR-L1 - human
 N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6
 C:Species: Homo sapiens (man)
 C:Date: 31-Jan-1997 #sequence revision 31-Jan-1997 #text_change 09-Jul-2004
 R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 Biochem. Biophys. Res. Commun. 227: 846-853, 1996
 Article: Molecular cloning and RNA expression of two new human chemokine receptor-like 9
 A:Reference number: JCS067; MUID:97040707; PMID:8886020
 A:Accession: JCS067
 A:Molecule type: DNA
 A:Residues: 1-355 <ZAB>
 A:Cross-references: UNIPROT:P51685; EMBL:279782; NID:91668735; PIDN:CAB021142.1; PID:9166
 R;Napolitano, M.; Zingon, A.; Bernardini, G.; Spinetti, G.; Rochchi, M.; Santoni, A.
 Submitted to the EMBL Data Library, June 1996
 A:Reference number: H01714
 A:Accession: G02776
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: DNA

A:Residues: 1-355 <NPAP>
 A:Cross-references: EMBL:U62555; NID:91468978; PID:91468979
 R:Bonner, T.I.
 Submitted to the EMBL Data Library, January 1996
 A:Reference number: H01154
 A:Accession: G0387
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-355 <BON>
 A:Cross-references: EMBL:U45983; NID:91245057
 C:Comment: This protein belongs to the family of beta chemokine receptors.
 C:Genetics:
 A:Gene: GDB:CMKBR8; OMKBRL2; TBR1; CKR-L1
 A:Cross-references: GDB:6053733; OMIM:601834
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 P:36-63/Domain: transmembrane #status predicted <TM1>
 P:73-94/Domain: transmembrane #status predicted <TM2>
 P:108-129/Domain: transmembrane #status predicted <TM3>
 P:147-171/Domain: transmembrane #status predicted <TM4>
 P:200-222/Domain: transmembrane #status predicted <TM5>
 P:39-260/Domain: transmembrane #status predicted <TM6>
 P:281-304/Domain: transmembrane #status predicted <TM7>
 Query Match 36.7%; Score 723; DB 2; Length 355;
 Best Local Similarity 43.5%; Pred. No. 1.e-55;
 Matches 131; Conservative 59; Mismatches 103; Indels 8; Gaps 3;
 Matches 137; Conservative 59; Mismatches 92; Indels 6; Gaps 3;

Qy 20 VTFFDYDY---GAPECHKFVDVKQIGAQOLPPPLYSVIFGFPGVGNMLUVLLILNCKLKC 75
 Db 9 VTTVDYDYPDIFSSPDABELQTNGKLLAVFYCLFVSLIGNSLNIVLVUVCKLRS 68

Qy 76 LTDIVLUNLAISDLLFLITLPLWAHSANENVFGNAMCKLFTGLYHIGYFGGIFFILLTIDRYLAIV 135
 Db 69 ITDVYLNLAISDLPFSPFPQTYLIDQWVFGTVCKVSVGFYTGFSMFFFTLMS 128

Qy 136 IDRYLAIVHAYVALKARTVTFGVTSVITLVAVASVPG31IFTKQKEDSVVVGPFYFP 195
 Db 129 VDRYLAIVHAYVALKARTVTFGVTSVITLVAVASVPG31IFTKQKEDSVVVGPFYFP 188

Qy 196 R---GWNNFHTIMRNILGLVPLLMICVYCSGILKTLRCRNEKRRRAVVFIMIVY 252
 Db 189 QQTWKWIKTNFKMNIGLILPFTYPCYKILHQKCONHKT KAIRLVLLIVVIAS 247

Qy 233 FUFWTPTNIVLNTFQBFEGLSNCESTSOLDQATOVTETLGTMTHCCINPIIYAFVGKFR 312
 Db 248 LLFWWPFPNVVFLTSLSMHLGDGSSISQQLTYATHTEIISFTHCCVNPIVIAFVGKFR 307

Qy 313 R 313
 Db 308 K 308

RESULT 13

JCS067 probable G protein-coupled receptor - rat
 N;Alternate names: Rattus norvegicus (Norway rat)
 C:Species: Rattus norvegicus
 C:Accession: 158186
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 R:Harrison, J. K.; Barber, C.M.; Lynch, K. R.
 Neurosci. Lett. 169, 85-89, 1994
 Article: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and brain
 A:Reference number: 158186; MUID:94323113; PMID:8047298
 A:Accession: 158186
 A:Molecule type: mRNA
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Residues: 1-354 <RES>
 A:Cross-references: UNIPROT:P35411; EMBL:U04808; NID:92558635; PIDN:AAE87093.1; PID:g439f
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor
 C:Query Match 35.8%; Score 704.5; DB 2; Length 354;

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BY BEST AVAILABLE COPY

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Result No.	Score	Query Match Length	DB ID	Description
1	1970	100.0	374	1 CCR2_HUMAN
2	1614.5	82.0	360	1 CCR2_MACMULAN
3	1346.5	68.4	373	1 CCR2_RAT
4	1327.5	67.6	373	1 CCR2_MOUSE
5	1252	67.4	373	2 Q6YTM12
6	1247	63.6	352	2 Q95NC2
7	1244	63.1	339	2 Q6GZB8
8	1244	63.1	339	2 Q9TQ73
9	1244	63.1	339	2 Q9TQ73
10	1244	63.1	352	2 Q6WN98
11	1244	63.1	352	2 Q9M2A0
12	1244	63.1	354	1 CCR5_MOUSE
13	1243	63.1	339	2 Q9TQ75
14	1243	63.1	352	2 Q95NC4
15	1241	63.0	352	2 Q6RN93
16	1241	63.0	352	2 Q6WN96
17	1241	63.0	352	2 Q6WN97
18	1240	62.9	339	2 Q9TUV0
19	1239	62.9	352	2 Q6YTA1
20	1239	62.9	352	2 Q9M293
21	1238.5	62.9	339	2 Q9TUV6
22	1238	62.8	339	2 Q9TUV1
23	1237	62.8	339	2 Q9TUV9
24	1236	62.7	339	2 Q9TQH0
25	1236	62.7	352	1 CCR5_CERTO
26	1236	62.7	352	1 CCR5_HYLLE
27	1236	62.7	352	2 Q8HZ79
28	1236	62.7	352	2 Q6WN92
29	1236	62.7	352	2 Q6WN94
30	1236	62.7	352	2 Q71RS2
31	1235	62.7	339	2 Q9TSN3

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OM protein - protein search, using SW model

Run on: June 9, 2005, 16:28:38 ; Search time 115.665 Seconds
(without alignments)

Title: US-10-791-166-2

Perfect score: 1655.798 Million cell updates/sec

Sequence: 1 MLSTSSRPFIRNTNEEVEV.....GKGSITGRAPEASLQDKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$

Maximum Match 100%

Listing first 45 summaries

Database : UniProt-03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1970	100.0	374	1 CCR2_HUMAN
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7	1244	63.3	354	2 Q6GZB8
8	1244	63.1	339	2 Q9TQ73
9	1244	63.1	339	2 Q9TQ73
10	1244	63.1	352	2 Q6WN98
11	1244	63.1	352	2 Q9M2A0
12	1244	63.1	354	1 CCR5_MOUSE
13	1243	63.1	339	2 Q9TQ75
14	1243	63.1	352	2 Q95NC4
15	1241	63.0	352	2 Q6RN93
16	1241	63.0	352	2 Q6WN97
17	1241	63.0	352	2 Q6WN98
18	1240	62.9	339	2 Q9TUV0
19	1239	62.9	352	2 Q6YTA1
20	1239	62.9	352	2 Q9M293
21	1238.5	62.9	339	2 Q9TUV6
22	1238	62.8	339	2 Q9TUV1
23	1237	62.8	339	2 Q9TUV9
24	1236	62.7	339	2 Q9TQH0
25	1236	62.7	352	1 CCR5_CERTO
26	1236	62.7	352	1 CCR5_HYLLE
27	1236	62.7	352	2 Q8HZ79
28	1236	62.7	352	2 Q6WN92
29	1236	62.7	352	2 Q6WN94
30	1236	62.7	352	2 Q71RS2
31	1235	62.7	339	2 Q9TSN3

RESULT 1		CRR2_HUMAN		STANDARD:
ID	P41597;	PRINTER:	PRINTER:	PRINTER: 374 AA.
AC	P41597;	PRINTER:	PRINTER:	PRINTER: 374 AA.
DT	01-NOV-1995 (Rel. 32, Created)	PRINTER:	PRINTER:	PRINTER: 374 AA.
DT	01-NOV-1995 (Rel. 32, Last annotation update)	PRINTER:	PRINTER:	PRINTER: 374 AA.
DT	25-OCT-2004 (Rel. 45, Last annotation update)	PRINTER:	PRINTER:	PRINTER: 374 AA.
DB	C-C chemokine receptor type 2 (C-C CCR-2) (CCR-2)	PRINTER:	PRINTER:	PRINTER: 374 AA.
DB	(Monocyte chemoattractant protein 1 receptor) (MCP-1-R).	PRINTER:	PRINTER:	PRINTER: 374 AA.
GN	Name=CCR2; Synonyms=CMKBR2;	PRINTER:	PRINTER:	PRINTER: 374 AA.
OS	Homo sapiens (Human).	PRINTER:	PRINTER:	PRINTER: 374 AA.
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	PRINTER:	PRINTER:	PRINTER: 374 AA.
NCBI_TaxID	9606;	PRINTER:	PRINTER:	PRINTER: 374 AA.
[1]	SEQUENCE FROM N.A. MEDLINE:94159821; PubMed:8146186;	PRINTER:	PRINTER:	PRINTER: 374 AA.
RA	Charo I.-F., Myers S.J., Herman A., Connolly A.J., Coughlin S.R.;	PRINTER:	PRINTER:	PRINTER: 374 AA.
RA	"Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternative splicing of the carboxyl-terminal tails.", Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).	PRINTER:	PRINTER:	PRINTER: 374 AA.
RA	SEQUENCE FROM N.A. MEDLINE:9415942; PubMed:8048929;	PRINTER:	PRINTER:	PRINTER: 374 AA.
RA	Yanagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.; "DNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor.", Biophys. Res. Commun. 202:1156-1162(1994).	PRINTER:	PRINTER:	PRINTER: 374 AA.
RA	SEQUENCE FROM N.A. MEDLINE:97150864; PubMed:8935400; DOI=10.1074/jbc.272.2.1038; Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.-F.; "Organization and differential expression of the human monocyte chemoattractant protein 1 receptor gene. Evidence for the role of the carboxyl-terminal tail in receptor trafficking.", J. Biol. Chem. 272:1038-1045(1997).	PRINTER:	PRINTER:	PRINTER: 374 AA.
RA	SEQUENCE FROM N.A. McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Parnell L., Dediha M., Ansari A., Marias E., Schutz K., Gnoj L., La Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watamabe M., Doggett N., Sagripanti J.L.; "Submission (May-1997) to the EMBL/GenBank/DDBJ databases.", J. Mol. Biol. 272:1038-1045(1997).	PRINTER:	PRINTER:	PRINTER: 374 AA.
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RL	Submitted (SPP-2002) to the EMBL/GenBank/DDBJ databases.
RN	[6] Sulfation of Tyr-26, and N-glycosylation.
RP	FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
RX	MEMLINE=20501139; PubMed=1046056;
RA	Preobrazhensky, A.A.; Dragan, S.; Kawano, T.; Gavrilin, M.A.; Galina, I.V., Chakravarty, L.; Kolattukudy, P.E.;
PA	"Monocyte chemoattractant protein-1 receptor CCR2B is a glycoprotein that has tyrosine sulfation in a conserved extracellular N-terminal region," J. Immunol. 165:5295-5303 (2000).
CC	-1- Transduces a signal by increasing the intracellular calcium ions level. Alternative coreceptor with CD4 for HIV-1 infection.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1- ALTERNATIVE PRODUCTS: Integral membrane protein.
CC	Name=A;
CC	ISO-Id=P41597-1; Sequence=Displayed;
CC	Name=B;
CC	ISO-Id=P41597-2; Sequence=VSP_001893;
CC	-1- PTM: N-glycosylation.
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR	ENB1; U03882; AAA19119.1; -.
DR	ENB1; U03905; AAA19120.1; -.
DR	D29784; BA0253.1; -.
DR	EMBL; AAC51637.1; -.
DR	EMBL; U80924; AAC51636.1; -.
DR	EMBL; U95626; AA857791.1; -.
DR	EMBL; U95626; AA857792.1; -.
DR	EMBL; AF545480; AAH16300.1; -.
DR	P1R; I38450; I38455.
DR	JC2443; JC2443.
DR	PDB; 1KAD; Model; A=1-349.
DR	PDB; 1KP1; Model; A=1-349.
DR	GeneID: HGNC:1603; CCR2.
DR	MINM; 601267; -.
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.
DR	GO; GO:0006515; C:soluble fraction; TAS.
DR	PDB; 1KAD; Model; A=1-349.
DR	GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .); TAS.
DR	GO; GO:0006948; P:cellular defense response; TAS.
DR	GO; GO:0006935; P:chemotaxis; TAS.
DR	GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR	GO; GO:0006554; P:inflammatory response; TAS.
DR	GO; GO:0007259; P:JAK-STAT cascade; TAS.
DR	GO; GO:007194; P:negative regulation of adenylylate cyclase ac. . .; TAS.
DR	InterPro; IPR00055; Chmkine receptor.
DR	InterPro; IPR000276; GPCR_Rhodopen.
DR	PRINTS; PR00237; GPCR_RHODOPSN.
DR	PROSITE; PS00237; G_protein_Recep_F1_1; 1.
DR	PROSITE; PS50262; G_protein_Recep_F1_2; 1.
KW	3D-structure; Alternative splicing; Glycoprotein; Polymorphism; Sulfation; Transmembrane.
FT	TRANSMEM DOMAIN 1 42 Extracellular (Potential).
FT	TRANSMEM DOMAIN 70 1 (Potential).
FT	TRANSMEM DOMAIN 71 80 Cytoplasmic (Potential).
FT	TRANSMEM DOMAIN 81 100 2 (Potential).
FT	TRANSMEM DOMAIN 101 114 Extracellular (Potential).
FT	TRANSMEM DOMAIN 115 136 3 (Potential).
FT	TRANSMEM DOMAIN 137 153 Cytoplasmic (Potential).
FT	TRANSMEM DOMAIN 154 178 4 (Potential).
FT	TRANSMEM DOMAIN 179 206 Extracellular (Potential).
FT	TRANSMEM DOMAIN 207 226 5 (Potential).
FT	TRANSMEM DOMAIN 227 243 Cytoplasmic (Potential).
FT	TRANSMEM DOMAIN 244 268 6 (Potential).
FT	TRANSMEM DOMAIN 269 285 Extracellular (Potential).
FT	TRANSMEM DOMAIN 286 309 7 (Potential).
FT	TRANSMEM DOMAIN 310 374 Cytoplasmic (Potential).
FT	CARBONYD 14 14 N-linked (GlcNAc. . .) (Potential).
FT	MOD RES 26 26 Sulphotyrosine.
FT	DISULFID 113 190 By similarity.
FT	VARSPLIC 314 374 SLTHIAUGCRIAPLQQPKVCGGPQVRPGKVNKVTTQGLDGR QCKSGKSRGAPESLQDEGKA -> RYTSVFFRKHRTRFRCK (isoform B).
FT	VARIANT 64 64 V->I (in dbSNP 101893).
FT	VARIANT 355 355 G -> E.
FT	SEQUENCE 374 AA; 41914 MW; F865BD39E74CF0 CRCG64;
Query Match	100.0%; Score 1970; DB 1; Length 374;
Best Local Similarity	100.0%; Pred. No. 1e-118;
Matches	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MUSTSRSPRINTNESGEVTTEFDYDYGAPCHKEVKIGAQQLPLPOLYSLYVPIFGVGN 60
Db	1 MUSTSRSPRINTNESGEVTTEFDYDYGAPCHKEVKIGAQQLPLPOLYSLYVPIFGVGN 60
Qy	61 MLVVLLINCKLKLCIDTYLLNLAIASDPLFLITLPLWAHSANNEWFGNAMCKLFGLY 120
Db	61 MLVVLLINCKLKLCIDTYLLNLAIASDPLFLITLPLWAHSANNEWFGNAMCKLFGLY 120
Qy	121 HIGYFG3IPFILLTITIDRYLAIVHAVALKARTVTFGVVTSVITWLAVAFASVPGIIFTK 180
Db	121 HIGYFG3IPFILLTITIDRYLAIVHAVALKARTVTFGVVTSVITWLAVAFASVPGIIFTK 180
Qy	181 CQKEDSYTYVCGPFPRGNNFNTIMRNILGVLPLLMIVCYSGILAKTLRCRNEKCRHR 240
Db	181 CQKEDSYTYVCGPFPRGNNFNTIMRNILGVLPLLMIVCYSGILAKTLRCRNEKCRHR 240
Qy	241 AVRVIITIMIVFLFWPYNIVILLNFOEFPLNSCESTDQDQTQVTEITGMTCII 300
Db	241 AVRVIITIMIVFLFWPYNIVILLNFOEFPLNSCESTDQDQTQVTEITGMTCII 300
Qy	301 NPPIYAFGEKERSLSLFIHALGCRIPQKPVCGGPGRGPQKVNKVTTQGLDGRGKRSI 360
Db	301 NPPIYAFGEKERSLSLFIHALGCRIPQKPVCGGPGRGPQKVNKVTTQGLDGRGKRSI 360
RESULT 2	
CCR2_MACMU	STANDARD; PRT; 360 AA.
ID CCR2_MACMU	018793;
AC	018793;
DT	16-OCT-2001 (Rel. 1.40, Created)
DT	16-OCT-2001 (Rel. 1.40, Last sequence update)
DT	25-OCT-2004 (Rel. 1.45, Last annotation update)
DE	C-C chemokine receptor type 2 (C-C CR2) (CC-CR2)
DE	(Monocyte chemoattractant protein 1 receptor)
GN	Name=CCR2; Synonyms=CNKBR2;
OS	Macaca mulatta (Rhesus macaque).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC	Cercopithecinae; Macaca.
OX	NCBI_TaxID=9544;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	Medline=21354156; PubMed=11461684; DOI=10.1089/088922201750290104;
RA	Margulies B.J.; Hauer D.A.; Clements J.B.;
RT	"Identification and comparison of eleven rhesus macaque chemokine

RT receptors";		Db 241 AVRIFTIMIVYFLFWTPNIVILNTFQEFFGLSNCESTRQDQATQVTTGTMTHCCI 300
RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).		
CC -1- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.		
CC -1- Transduces a signal by increasing the intracellular calcium ions level.		
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC -1- ALTERNATIVE PRODUCTS:		
CC Event=Alternative splicing; Named isoforms=2;		
CC Name=B;		
CC IsoId=OL8793-1; Sequence=displayed;		
CC Name=A;		
CC IsoId=OL8793-2; Sequence=Not described;		
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.		
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC EMBL: AP013958; AA011572; 1; -		
DR InterPro; IPR002237; CC_2 receptor.		
DR InterPro; IPR000355; Chkine receptor.		
DR InterPro; IPR000276; GPCR_Rhodopsin.		
DR Pfam; PF00001; 7tm_1; 1.		
DR PRINTS; PR00237; G PROTEIN RECEPTOR_F1_1; 1.		
DR PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1; 1.		
DR PROSITE; PS00262; G PROTEIN RECEPTOR_F1_2; 1.		
KW Alternative splicing; G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.		
CC DOMAIN 1 42 Extracellular (Potential).		
FT DOMAIN 43 70 1 (Potential).		
FT DOMAIN 71 80 Cytoplasmic (Potential).		
FT TRANSMEM 81 100 2 (Potential).		
FT DOMAIN 101 114 Extracellular (Potential).		
FT TRANSMEM 115 136 3 (Potential).		
FT DOMAIN 137 153 Cytoplasmic (Potential).		
FT TRANSMEM 154 178 4 (Potential).		
FT DOMAIN 179 206 Extracellular (Potential).		
FT TRANSMEM 207 226 5 (Potential).		
FT DOMAIN 227 243 Cytoplasmic (Potential).		
FT TRANSMEM 244 268 6 (Potential).		
FT DOMAIN 269 285 Extracellular (Potential).		
FT TRANSMEM 286 309 7 (Potential).		
FT DOMAIN 310 360 Cytoplasmic (Potential).		
FT CARBOHYD 14 14 N-Linked (GlcNAc. . .) (Potential).		
FT DISTRIFID 26 26 Sulfonylurea (By similarity).		
FT SEQUENCE 360 AA; 41139 MW; 4B2552B0E911FEE9P CRC64;		
SQ		
Query Match Score 1614.5; DB 1; Length 360;		
Best Local Similarity 96.6%; Pred. No. 6.1e-96;		
Matches 308; Conservative 4; Mismatches 4; Indels 3; Gaps 1;		
Qy 1 MLSTSRSPRNTNESGEETTTPDYDGPCKPDKVQGAQLPLYSLVPIFGFTGN 60		
Db 1 MLSTSRSPRNTNESGEETTTPDYDGPCKPDKVQGAQLPLYSLVPIFGFTGN 60		
Qy 61 MLVVLILINKKGLKLTDLVLLNIAISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120		
Db 61 MLVVLILINKKGLKLTDLVLLNIAISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120		
Qy 121 HIGYGGIPFILLTIDRYIAIVHAFALKARTTYFGVVTSTVWVAVFASVPGIIFTK 180		
Db 121 HIGYGGIPFILLTIDRYIAIVHAFALKARTTYFGVVTSTVWVAVFASVGIIFTK 180		
Qy 181 CQEDSVTVCPPGRMNFIHTMNLIGVPLIMIVCYSSILKTILRCNEKEKRR 240		
Db 181 CQEDSVTVCPPGRMNFIHTMNLIGVPLIMIVCYSSILKTILRCNEKEKRR 240		
Qy 241 AVRIFTIMIVYFLFWTPNIVILNTFQEFFGLSNCESTRQDQATQVTTGTMTHCCI 300		

FT	DISULFID	126	203	By similarity.
SQ	SEQUENCE	373 AA;	42763 MW;	2E7B0125D6FD09 CRC64;
Query Match Score	68.4%;	Score 1346.5;	DB 1;	Length 373;
Best Local Similarity	76.9%;	Pred. No. 9.5e-79;		
Matches 257; Conservative 25;	Mismatches 45;	Indels 7;	Gaps 3;	
Qy	1	MLSTSRSPRINTNESGEETVTFDFDYGAPECHKFVKQIGQLPPLPLSIFTFGFGVGN	60	CC
Db	14	ILSTSHSLPFSIQELDEGATTPYDDGEPCHKTSTVKQIGAWILPPLSIFTFGFGVGN	73	CC
Qy	61	MVLVLLINCKKLCIKLTDIYLNLASDLFLFLTLPWAHAAANEVFGNAMCKLFTGLY	120	CC
Db	74	MVLVLLISCKLKSKMNDIYFNLAISDLFLFLTLPWAHAAANEVFGNAMCKLFTGLY	133	CC
Qy	121	HIGYFGGIFTFLLTDRYLAVTAHVAFALKARTVTGVSFTSVTMLVAFASVPGIFTK	180	CC
Db	134	HIGYFGGIFTFLLTDRYLAVTAHVAFALKARTVTGVSFTSVTMLVAFASVPGIFTK	193	CC
Qy	181	COKEDSYVVCGPYFPGRWNNTPTIMENILGLVPLLMIVCYSGILKTLRCRNEKRHR	240	CC
Db	194	SEQEDQHTCSPYFPITWNQTIMANLSSLLPLMIVCYSGILKTLRCRNEKRHR	253	CC
Qy	241	AVRVFTIMIVYFLFPTPNVXVILANTFOEGFLSNCESITSOLOAQQTFLGTHCCCI	300	CC
Db	254	AVRLPAIMIVYFLFPTPNVTLFLTFOETGMNSNCVVDHLDQAMQVTTLGHMTHCCV	313	CC
Qy	301	NPIIYAFVGEBKFR--SLF--HIALG-CRAPL	327	CC
Qy	314	NPIIYAFVGEBKFR--SLF--HIALG-CRAPL	347	CC
Db	314	NPIIYAFVGEBKFR--SLF--HIALG-CRAPL	347	CC
RESULT 4				
CCR2_MOUSE				
ID	PS51633; Q61172;	STANDARD;	PRT;	373 AA.
AC	P51633; Q61172;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DT	25-OCT-2014 (Rel. 45, Last annotation update)			
DB	C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2)			
DE	(JE/SIC receptor) (MCP-1 receptor).			
GN	Name=Ocr2; Synonyms=cmkb2;			
OS	Mus musculus (Mouse); Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10030;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9205938; PubMed=863187; DOI=10.1074/jbc.271.13.7551;			
RA	Boring L., Gosling J., Monteciaro F.S., Luisi A.J., Tsou C.-L., Charo I.F., Heeschen M., Tanaka M.A., Yoshizawa T., Liu Y., Klin R., Post T.W., Gerard C., Dorf M.R.;			
RT	"Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein 1alpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9." ; J. Biol. Chem. 271:7551-7558 (1996).			
RT	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c;			
RX	MEDLINE=9216064; PubMed=8662823; DOI=10.1074/jbc.271.20.11603;			
RA	Kurihara T., Bravo R.;			
RT	"Cloning and functional expression of mCCR2, a murine receptor for the C-C chemokines JE and FIC".			
RL	J. Biol. Chem. 271:11603-11606 (1996).			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91026720; PubMed=8872298;			
RA	DOI=1.0-10.2160/ (SICR)1097-4547(19960815)45:4<382::AID-JNR7>3.0.CO;2-H;			
RA	"Heeschen M., Tanaka M.A., Berman S., Yoshizawa T., Liu Y., Klin R., Post T.W., Gerard C., Dorf M.R.;			
RA	Post T.W., Gerard C., Dorf M.R.;			
RT	"Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse transcriptase-polymerase chain reaction does not detect mRNA for the KC or new MCP-1 receptor.";			
Qy	[3]			
Db	SEQUENCE FROM N.A.			
RX	1 MLSTSRSRFIRNTNESEGEETVTFDYYGAPCHKFKDVRQIGAQOLPLPLSIFTFGFVGN	61	MLVLLINCKKLKCLTDIYLNIAISDPLLELTPLWMAHSAANEWFGNAMKLFGTGLY	120
RA	"Cloning and functional expression of mCCR2, a murine receptor for the C-C chemokines JE and FIC".	74	MLVLLIIGCKLKSMTDIYLNIAISDPLLELTPLWHAHYANEWFGNIMKVFVGLY	133
Qy	[3]			
Db	SEQUENCE FROM N.A.			
RX	1 MLVLLIINGCKLCLTDIYLNIAISDPLLELTPLWMAHSAANEWFGNAMKLFGTGLY	60	HIGYFGGIFTFLLTDRYLAVTAHVAFALKARTVTGVSFTSVTMLVAFASVPGIFTK	180
RA	DOI=1.0-10.2160/ (SICR)1097-4547(19960815)45:4<382::AID-JNR7>3.0.CO;2-H;	75	14 ILSTSHSLTRSIQELDGGATPYDDGEGPKHTSQRQIGAMILPLPLSIFTFGFVGN	193
RA	"Heeschen M., Tanaka M.A., Berman S., Yoshizawa T., Liu Y., Klin R., Post T.W., Gerard C., Dorf M.R.;			
RA	Post T.W., Gerard C., Dorf M.R.;			
RT	"Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse transcriptase-polymerase chain reaction does not detect mRNA for the KC or new MCP-1 receptor.";			

Qy	196	RG---WNNFTIMRNILGLVPLILMVTCYSGILKTKLIRCRNKEKRRAVRVIFTIMIV	251	Matches	233;	Conservative	29;	Mismatches	40;	Indels	6;	Gaps	2;
Db	184	FGQYRWNQKLTMMVILGLVPLILMVTCYSGILKTKLIRCRNKEKRRAVRVIFTIMIV	243	Qy	17	GEEVTTFEDDYD--GAPECHKFVDVKOIGAQOLIPLPLSISVIFGEGVNMNLAVLILNCCLK	74						
Db	252	YFLWPTPYNIVILLNTQFOEFGNSCESTSQDQATOVTETLGTMHCCINPIIYAFGEK	311	Db	5	GSIPTYTYDIDMSMAPQKENVQIQIAQLEPLYSVIFGEGVNMNLAVLILNCCLK	64						
Db	244	YFLWAPINVILLNTQFOEFGINNCSSSNRLQAMQVTEITLGTMHCCVNPPIIYAFGEK	303	Qy	75	CLEDIYLNLASDLLELITLPLWAHSAAANEVFGNAMCKLFPGLYHGTYEGGIEFFILL	134						
Qy	312	FRSLF----HIA 319		Db	65	SMDIYLFNLASDLLELITLPLWAHSAAANEVFGNAMCKLFPGLYHGTYEGGIEFFILL	124						
Db	304	FRNYLLVFPQKHTA 317		Qy	135	TIDRYLAHVAFALKARTVTFGVTMVAVASVPGLIFTKCQEDSVVCCGPYF	194						
Db	Q68G28	PRELIMINARY;	PRT;	Db	125	TIDRYLAHVAFALKARTVTFGVTMVAVASVPGLIFTKCQEDSVVCCGPYF	184						
RESULT 7													
Q68G28				Qy	195	P---RGNNNFHTIMRNILGLVPLILMVICSGILKTKLIRCRNKEKRRAVRVIFTIMI	250						
ID	Q68G28;	PRELIMINARY;	PRT;	Db	185	PRQYRWTKHFOQLKOMTSLPLIPLWVYCIGLNLTLFRCRNKEKRRAVRVIFTIMI	244						
AC	Q68G28;			Qy	251	VYFLFWTPYNTVILLNTQEFFGLNSCESTSQDQATOVTETLGTMHCCINPIIYAVG	310						
DT	25-OCT-2004	(TREMBLrel.	28;	Db	245	VYFLFWTPYNTVILLNTQEFFGLNSCESTSQDQATOVTETLGTMHCCINPIIYAVG	304						
DT	25-OCT-2004	(TREMBLrel.	28;	Qy	311	KPRLFH1 318							
DT	25-OCT-2004	(TREMBLrel.	28;	Db	305	KFNYLSV 312							
DR	Chemokine (C-C) receptor 5.												
GN	Name=Cmbr5;												
GN	Rattus norvegicus (Rat).												
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.												
OX	NCBI_TaxID=10116;												
RN	[1]	SEQUENCE FROM N.A.											
RP	TISSUE=Kidney;												
RC	PubMed=12477932;	DOI=10.1073/pnas.242603899;											
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,												
RA	Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schulter G.D.,												
RA	Altschul S.F., Zobell K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,												
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,												
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,												
RA	Singleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,												
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,												
RA	Rosa S.A., Loqueilano N., Peters G.J., Abramson R.D., Mulilaty S.J.,												
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,												
RA	Villalba D.J., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,												
RA	Fahay J., Heitton E., Kettenman M., Madan A., Rodriguez S., Sanchez A.,												
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,												
RA	RA DR	Touchman J.W., Green B., Dickson D., Myers R.M., Butterfield Y.S.,											
RA	Rodriguez A.C., Grimes R.M., Schmitz J.M., Myer C.,												
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.B.,												
RA	Jones S.J., Marra M.A., Generation and initial analysis of more than 15,000 full-length human												
RT	RT	RT											
RT	RT	RT											
RL	RL	RL											
RN	[2]	SEQUENCE FROM N.A.											
RP	TISSUE=Kidney;												
RC	Director MGC Project;												
RA	Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.												
RL	DR GO; GO:004872; F:receptor activity; IEA.												
DR	InterPro; IPR000923; BlueCu_1.												
DR	InterPro; IPR000355; Chmkine receptor.												
DR	InterPro; IPR000276; GPCR_Rhodopsin.												
DR	PFam; PF00001; 7cm_1; 1.												
DR	PRINTS; PRO0057; CCHEMOKINER.												
DR	PRINTS; PRO0237; GPCR_RHODOPSIN.												
DR	PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.												
DR	PROSITE; PS00237; G_PROTEIN_REC_EF1_1; UNKNOWN_1.												
DR	PROSITE; PS50262; G_PROTEIN_REC_EF1_2; 1.												
KW	Receptor.												
SEQUENCE	354 AA;	41081 MW;	4CCB9A9C4EBE985C CRC34;										
SQ	Query Match Score 63.3%; Pred. No. 2.e-29;	Score 1247; DB 2;	Length 354;										
Best Local Similarity	75.6%;	Pred. No. 2.e-29;											

Query Match Score 63.3%; Pred. No. 2.e-29;
 Best Local Similarity 75.6%;

IEA; InterPro; IPR000923; BlueCu_1.

GO; GO:0004872; F:receptor activity; IEA.
 GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 GO; GO:10007186; P:G-protein coupled receptor protein signalin. . . IEA.
 InterPro; IPR000923; BlueCu_1.

DR	InterPro; IPR002240; CC_5 receptor.	CC	-1 - SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR	InterPro; IPR003355; Chmkine receptor.	CC	-1 - SIMILARITY: Belongs to Family 1 of G-protein coupled receptors.
DR	InterPro; IPR00276; GPCR_Rhodpsn.	DR	EMBL; AF161929; AD4766.1; -.
DR	PRINTS; PR000657; CCHEMOKINER.	DR	GO; GO:0016021; C:internal to membrane; IEA.
DR	PRINTS; PR01110; CHEMOKINERS.	DR	GO; GO:0016433; F:G-C-C chemokine receptor activity; IEA.
DR	PRINTS; PR00237; GCRRHODOPSN.	DR	GO; GO:0004872; P:receptor activity; IEA.
DR	PROSITE; PS00196; COPPER BLUE; UNKNOWN_1.	DR	GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR	PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1; 1.	DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR	PROSITE; PS50262; G PROTEIN RECEPTOR_F1_2; 1.	DR	InterPro; IPR00923; BlueCu_1.
KW	G-protein coupled receptor; Receptor; Transmembrane.	DR	InterPro; IPR002240; CC_5 receptor.
FT	NON_TER 1	DR	InterPro; IPR00355; Chmkine receptor.
FT	NON_TER 1	DR	InterPro; IPR00276; GPCR_Rhodpsn.
SQ	SEQUENCE 339 AA; 339 390 MN; C1313952B71B50C7 CRC64;	DR	PRINTS; PR00657; CCHEMOKINER.
	Query Match 63.1%; Score 124.4; DB 2; Length 339;	DR	PRINTS; PR01110; CHEMOKINERS.
	Best Local Similarity 76.6%; Pred. No. 3.3e-72;	DR	PRINTS; PR00237; GCRRHODOPSN.
Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;		DR	PROSITE; PS00196; COPPER_BIUE; UNKNOWN_1.
QY	24 FDYDG--APCHKFDVKQIGAQQLPPLYSVLPFSGVGNMLVYLINCKKLKCLTDYL 81	DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
Db	: : 3 YDIDGPSSBCRKDKQMGAAHLLPPLYSVLPFSGVGNMLVYLINCKKLKCLTDYL 62	DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
QY	82 LNLAISDLFLITPLWAHSAAANEWFGNAMCKLFTGLXHIGPGGIPSTILLTDRYLA 141	DR	G-protein coupled receptor; Receptor; Transmembrane.
Db	63 LNLAISDLFLITPLWAHSAAANEWFGNAMCKLFTGLXHIGPGGIPSTILLTDRYLA 122	FT	NON_TER 1
QY	142 IVHAVFAALKARTVTFGVVTSVTHLVAVPASVPGIITPKQEDVYGPYPF---RG 197	FT	NON_TER 1
Db	123 IVHAVFAALKARTVTFGVVTSVTHLVAVPASVPGIITPKQEDVYGPYPF---RG 182	SEQUENCE	339 AA; 339 390 MN; 6A67CF5D22C70C49 CRC64;
QY	198 WNNFTTIMINLGLVPLJLMIVCYSGLKLTKLJCRNECKRHRVAVRVTIMIVYFLWT 257	QY	Query Match 63.1%; Score 124.4; DB 2; Length 339;
Db	183 WNNFTTIMINLGLVPLJLMIVCYSGLKLTKLJCRNECKRHRVAVRVTIMIVYFLWT 242	DR	Best Local Similarity 77.3%; Pred. No. 3.3e-72;
QY	258 PYNIVLILANTQEQFFGLNSCCESTSQLDQATQVETLGMTICCINPIIYAFVGKEFRSLF- 316	DR	Mismatches 24; Indels 12; Gaps 3;
Db	243 PYNIVLILANTQEQFFGLNSCCESTSQLDQATQVETLGMTICCINPIIYAFVGKEFRNLIA 302	DR	YDIDGPSSBCRKDKQMGAAHLLPPLYSVLPFSGVGNMLVYLINCKKLKCLTDYL 62
QY	317 ----HIA 319	DR	LNLAISDLFLITPLWAHSAAANEWFGNAMCKLFTGLXHIGPGGIPSTILLTDRYLA 141
Db	303 VFFQKHIA 310	Db	LNLAISDLFLITPLWAHSAAANEWFGNAMCKLFTGLXHIGPGGIPSTILLTDRYLA 122
RESULT 9	Q9TUUV8 PRELIMINARY; PRT; 339 AA.	QY	FDYDG--APCHKFDVKQIGAQQLPPLYSVLPFSGVGNMLVYLINCKKLKCLTDYL 81
Q9TUUV8	PRELIMINARY; PRT; 339 AA.	Db	YDIDGPSSBCRKDKQMGAAHLLPPLYSVLPFSGVGNMLVYLINCKKLKCLTDYL 62
AC	NCBI_TaxID=100754;	Q6WN98	LNLAISDLFLITPLWAHSAAANEWFGNAMCKLFTGLXHIGPGGIPSTILLTDRYLA 141
DT	01-MAY-2000 (TREMBrel. 13, Created)	ID	Q6WN98; PRELIMINARY; PRT; 352 AA.
DT	01-MAY-2000 (TREMBrel. 13, Last sequence update)	AC	Q6WN98; PRELIMINARY; PRT; 352 AA.
DT	01-MAR-2004 (TREMBrel. 26, Last annotation update)	DT	05-JUL-2004 (TREMBrel. 27, Created)
DE	C-C Chemokine receptor 5 (Fragment).	DT	05-JUL-2004 (TREMBrel. 27, Last sequence update)
GN	Name=CCRS5;	DE	25-OCT-2004 (TREMBrel. 28, Last annotation update)
OS	Saguinus sp.	GN	Name=ccr5;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.	OS	Calithrix humeralifera (Tassel-eared marmoset).
OX	NCBI_TaxID=100754;	ID	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Callithrix.
RN	SEQUENCE FROM N.A.	Q6WN98	Callithrix humeralifera (Tassel-eared marmoset).
RP	MEDLINE=12942991; PubMed=14581567;	AC	Callithrix humeralifera (Tassel-eared marmoset).
RX	DOI=10.1128/JVI.77.22.12318.2003;	DT	Callithrix humeralifera (Tassel-eared marmoset).
RA	Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R., Doms R.W., Marx P., Wolinsky S.M., Stanton J., Shabata R., Yoder A.D., Pillai S., Kunstman J., Stanton J., Agy M., Shabata R., Yoder A.D., Pillai S., Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shabata R., Yoder A., Pillai S., Kuijken C., Marx P., Wolinsky S.;	RA	Callithrix humeralifera (Tassel-eared marmoset).
RT	"Structure and function of Cc-chemokine receptor 5 homologues derived from representative primate species and subspecies of the taxonomic suborders Prosimi and Anthropoidea."	RA	Callithrix humeralifera (Tassel-eared marmoset).
RT	J. Virol. 77:12310-12318 (2003).	RA	Callithrix humeralifera (Tassel-eared marmoset).
RL	[2]	RA	SEQUENCE FROM N.A.
RN	SEQUENCE FROM N.A.	RP	Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
RP	MEDLINE=12942991; PubMed=14581567;	RA	SEQUENCE FROM N.A.
RX	DOI=10.1128/JVI.77.22.12318.2003;	RA	Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
RA	Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R., Doms R.W., Marx P., Wolinsky S.M., Stanton J., Shabata R., Yoder A.D., Pillai S., Kuijken C., Marx P., Wolinsky S.;	RA	SEQUENCE FROM N.A.
RT	"Structure and function of Cc-chemokine receptor 5 homologues derived from representative primate species and subspecies of the taxonomic suborders Prosimi and Anthropoidea."	RA	SEQUENCE FROM N.A.
RT	J. Virol. 77:12310-12318 (2003).	RA	SEQUENCE FROM N.A.
RN	SEQUENCE FROM N.A.	RA	Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
RP	"CCRS5 chemokine receptor gene evolution in new world monkeys (Platyrrhini, Primates): implication on resistance to lentiviruses."	RA	SEQUENCE FROM N.A.
RA	Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shabata R., Yoder A., Pillai S., Kuijken C., Marx P., Wolinsky S.;	RA	SEQUENCE FROM N.A.
RA	Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.	RA	SEQUENCE FROM N.A.
RL	Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.	RA	SEQUENCE FROM N.A.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AY278745; AAQ020013.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:004872; F:receptor activity; IEA.
 DR GO; GO:001584; F:G-protein coupled receptor protein activity; IEA.
 DR InterPro; IPR009323; BlueC1_1.
 DR GO; GO:007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
 DR InterPro; IPR002240; CC 5 receptor.
 DR InterPro; IPR00355; ChmkIne receptor.
 DR InterPro; IPR00276; GPCR_Rhodpsn.
 DR PRINTS; PR00001; 7tm 1..1.
 DR PRINTS; PR01110; CHEMOKINERS.
 DR PROSITE; PS00237; GPCR_RHODPSN.
 DR PROSITE; PS00196; COPPER_BLOU; UNKNOWN 1.
 DR PROSITE; PS000237; G_PROTEIN_RECEP_F1_1..1.
 DR PROSITE; PS05262; G_protein coupled receptor RECEP_F1_2..1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ 'SEQUENCE' 352 AA; 40522 MW; FP0D0A852B553AF5 CRC64;
 Query Match Score 1244; DB 2; Length 352;
 Best Local Similarity 76.6%; Pred. No. 3.4e-72;
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;
 Qy 24 FDYDG--APCHKEPDVKQIGAQQLPLPLSLVIFPGEVNMLVYLILINCKLKCLTDYL 81
 Db 10 YDIDYGPSPCRKLDVKQKGHLPLPLSMVFLFGEVNMLVYLILINCKLSMTDYL 69
 Qy 82 LNLAIASDLFLPLTLPLWAHSAANEWVFGNAQMCKLPLGLYHGYGGFEPPIIILITDYL 141
 Db 70 LNLAIASDLFLPLTLPLWAHSAAAGWDGFNTMCQFLTGlyFIGFGSGIFFILITDYL 129
 Qy 142 IVHAFALKARTTTFGVTSVITWLVAFAASVPGIIIFTKCQEDSVVYCGYPFP---RG 197
 Db 130 IVHAFALKARTTTFGVTSVITWLVAFAASLPGIIITRQSKEGYHTCSPHFFPSQVQF 189
 Qy 198 WNNFTHTMRNLTGHVYLPLIMIVCYSGIITKLTLLCRNEKKRHRVAVRIFTIMIVYELFWT 257
 Db 190 WKNFTETLKVNTKVLPLIMIVCYSGIITKLTLLCRNEKKRHRVAVRIFTIMIVYFLFWA 249
 Qy 258 PYNIVLANTPQBPFGLSNCESTSQSQLQATQTETLGTHCCNPIIYAFGEKFRLSLF- 316
 Db 250 PYNIVLANTPQBPFGLSNCESTSQSQLQATQTETLGTHCCNPIIYAFGEKFRLSLF- 309
 Qy 317 ----HIA 319
 Db 310 VFFOKHIA 317

CC differential haplotype-specific transcriptional activity, and altered translocation factor binding to polymeric nucleotides in the pathogenesis of HIV-1 and simian immunodeficiency virus.";
 DR EMBL; Chem. 275:18946-18961 (2000).
 RN 12] RSEQUENCE FROM N.A.
 RX MEDLINE-22174698; PubMed=12186836;
 RA LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
 RT "Blockade of HIV-1 infection of New World monkey cells occurs primarily at the stage of virus entry.";
 RT RT J. Exp. Med. 196:431-445 (2002).
 RN 13] RSEQUENCE FROM N.A.
 RP RSEQUENCES FROM E.A.J.M., Schrago C.G., Ribeiro I.P., Bissinatti A., Soares M.A.;
 RA Soanez H.N.; Russo C.A.M.; Tanuri A.; Soares M.A.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

[4] RSEQUENCE FROM N.A.
 RP Zhang Y., Ryder O.A., Zhang Y.;
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:004872; F:receptor activity; IEA.
 DR GO; GO:000262; G_protein coupled receptor RECEP_F1_2..1.
 DR GO; GO:001693; F:chemokine receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
 DR InterPro; IPR00276; CC 5 receptor.
 DR InterPro; IPR000240; CC 5 receptor.
 DR InterPro; IPR000355; ChmkIne receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR PRINTS; PR00001; 7tm 1..1.
 DR PRINTS; PR00657; C:CHEMOKINER.
 DR PRINTS; PR0110; CHEMOKINERS.
 DR PRINTS; PR0237; GPCR_RHODPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1..1.
 DR PROSITE; PS0262; G_protein_RECEP_F1_2..1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 352 AA; 40465 MW; FF0D0A8D067B885 CRC64;

Query Match Score 1244; DB 2; Length 352;
 Best Local Similarity 76.6%; Pred. No. 3.e-72;
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;

Qy 24 FDYDG--APCHKEPDVKQIGAQQLPLPLSLVIFPGEVNMLVYLILINCKLKCLTDYL 81
 Db 10 YDIDYGPSPCRKLDVKQKGHLPLPLSMVFLFGEVNMLVYLILINCKLSMTDYL 69
 Qy 82 LNLAIASDLFLPLTLPLWAHSAANEWVFGNAQMCKLPLGLYHGYGGFEPPIIILITDYL 141
 Db 70 LNLAIASDLFLPLTLPLWAHSAAAGWDGFNTMCQFLTGlyFIGFGSGIFFILITDYL 129
 Qy 142 IVHAFALKARTTTFGVTSVITWLVAFAASVPGIIIFTKCQEDSVVYCGYPFP---RG 197
 Db 130 IVHAFALKARTTTFGVTSVITWLVAFAASLPGIIITRQSKEGYHTCSPHFFPSQVQF 189
 Qy 198 WNNFTHTMRNLTGHVYLPLIMIVCYSGIITKLTLLCRNEKKRHRVAVRIFTIMIVYELFWT 257
 Db 190 WKNFTETLKVNTKVLPLIMIVCYSGIITKLTLLCRNEKKRHRVAVRIFTIMIVYFLFWA 249
 Qy 258 PYNIVLANTPQBPFGLSNCESTSQSQLQATQTETLGTHCCNPIIYAFGEKFRLSLF- 316
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 Qy 317 ----HIA 319
 Db 310 VFFOKHIA 317

RESULT 11
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 ID Q9MZA0
 AC Q9MZA0;
 DT 01-OCT-2000 (TREMBREL 15, Created)
 DT 05-JUL-2004 (TREMBREL 27, Last sequence update)
 DE CC chemokine receptor 5 (Chemokine receptor CCR5).
 GN Name=CCR5; Synonyms=ccr5;
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OC NCBI_TaxID=9483;
 RN 1] RSEQUENCE FROM N.A.
 RX MEDLINE-20317091; PubMed=10747879; DOI=10.1074/jbc.M000169200;
 RA Begum K., Galvis M.C., Kostecki V., Valente A.J., Murthy K.K.,
 RA Haro L., Dolan M.J., Allan J.S., Ahuja S.K.,
 RT "Evolution of human and non-human primate CC chemokine receptor 5 gene
 RT and mRNA. Potential roles for haplotype and mRNA diversity,"

Db	70	LNLALISDLILFLPTVFWAHTYAGWDGFNTMCQBLTGLYFIGFSGIFFLILITIDRYLA	129	Qy	142	IYHAFALKARTVFGVYTTSVITWLVAVFASVPGIIFTKQKEDSVYCGPYFPRG----	197
Qy	142	IYHAFALKARTVFGVYTTSVITWLVAVFASVPGIIFTKQKEDSVYCGPYFPRG----	197	Db	130	IYHAFALKARTVFGVYTTSVITWLVAVFASVPGIIFTKQKEDSVYCGPYFPRGOF	189
Db	130	IYHAFALKARTVFGVYTTSVITWLVAVFASVPGIIFTKQKEDSVYCGPYFPRGOF	189	Qy	198	WNNFTIMRNILIGVPLIIMVICYSGLIKLTLLCRNEKKRHRAVRIFTIMIVYFLWT	257
Qy	198	WNNFTIMRNILIGVPLIIMVICYSGLIKLTLLCRNEKKRHRAVRIFTIMIVYFLWT	257	Db	190	WNFPEALKARTVFGVYTTSVITWLVAVFASVPGIIFTKQKEDSVYCGPYFPRGOF	249
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Db	258	PYNVILANTQEFPGLSNCESTSQLDATQVETLGTHCCANPIIAFVGKEFKRSLE-	316	Qy	259	PYNVILLNTYQEFGLANCSSSNRLDQMVTETLGMTCCVNPIIAFVGKEFKRNYLV	309
Qy	259	PYNVILLNTYQEFGLANCSSSNRLDQMVTETLGMTCCVNPIIAFVGKEFKRNYLV	309	Db	317	-----HIA 319	317
Qy	317	-----HIA 319	317	Db	310	VFFRKHIA 317	310
Db	310	VFFRKHIA 317	310				
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				Job time : 117.165 secs			
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Q6WN93		PRELIMINARY;	PRM;	352 AA.			
ID	Q6WN93						
AC	Q6WN93;						
DT	05-JUL-2004	(TREMBLrel.	27,	Created)			
DT	05-JUL-2004	(TREMBLrel.	27,	Last sequence update)			
DT	05-JUL-2004	(TREMBLrel.	27,	Last annotation update)			
DE							
GN							
Name=ccr5;							
OS	Leontopithecus chrysopygus (Gold-and-black lion tamarin)						
OC	Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;						
OC	Leontopithecus						
OX	NCBI_TaxID=58710;						
RN							
RP	SEQUENCE FROM N.A. Soeira C.G., Ribeiro I.P., Pissinatti A.,						
RA	Soeira E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,						
RA	Souanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;						
RA	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.						
RL	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).						
CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.						
CC	EMBL: AY78750; ARQ2008.1. -						
DR	GO:0016021; C: integral to membrane; IEA.						
DR	GO: GO-0016493; F:C-C chemokine receptor activity; IEA.						
DR	GO: GO:004872; P: receptor activity; IEA.						
DR	GO: GO:001584; F: rhodopsin-like receptor activity; IEA.						
DR	DR: GO:0007186; B: G-protein coupled receptor protein signalin. . . ; IEA.						
DR	InterPro: IPR00933; BlueCu_1.						
DR	InterPro: IPR002240; CC_5 receptor.						
DR	InterPro: IPR000355; ChmkIne receptor.						
DR	InterPro: IPR00276; GPCR_Rhodpsn.						
DR	PFAM: PF00001; 7tm_1; 1.						
DR	PRINTS: PR000557; CCHEMOKINER.						
DR	PRINTS: PR01110; CHEMOKINERS.						
DR	PRINTS: PR00237; GPCR_RHODOPN.						
DR	PROSITE: PS00196; COPPER_B舅B; UNKNOWN_1.						
DR	PROSITE: PS00262; G PROTEIN RECEPTOR_F1_1; 1.						
KW	G-protein coupled receptor; Receptor; Transmembrane.						
SQ	SEQUENCE 352 AA; 40437 MW; SEC1884238503783 CRC64;						
Query Match	63.0%	Score 1241;	DB 2;	Length 352;			
Best Local Similarity	76.3%	Pred. No. 5.3e-72;					
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							Gaps 3;
Qy	24	PDYDGA--PCHRPDVKQIGAQOLPLPLVLFPGVGMMLVVLINCKLKQLTDIYL	81				
Db	10	YDIDYGASEPCKRDVKONGAHLLPLPLYSMVMVVLINCKRPSMTDYL	69				
Qy	82	LNLALISDLILFLPTVFWAHTYAGWDGFNTMCQBLTGLYFIGFSGIFFLILITIDRYLA	141				
Db	70	LNLALISDLILFLPTVFWAHTYAGWDGFNTMCQBLTGLYFIGFSGIFFLILITIDRYLA	129				

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OM protein - protein search, using SW model

Run on: June 9, 2005, 16:37:43 ; Search time 31.0817 seconds
(without alignments)

898.236 Million cell updates/sec

Title: US-10-791-166-2

Perfect score: 1970

Sequence: 1 MLSTSRSRIRNTNEGEEV.....GKGSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AN:
 1: /cgn2_6/.ptodata/1/1iaa/5A COMB.pep:
 2: /cgn2_6/.ptodata/1/1iaa/5B COMB.pep:
 3: /cgn2_6/.ptodata/1/1iaa/6A COMB.pep:
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 6: /cgn2_6/.ptodata/1/1iaa/backfile1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1970	100.0	374	1 US-08-450-393A-2	Sequence 2, Appli
2	1970	100.0	374	3 US-08-446-669-2	Sequence 2, Appli
3	1970	100.0	374	4 US-10-039-659A-14	Sequence 14, Appli
4	1970	100.0	374	4 US-09-625-573-2	Sequence 2, Appli
5	1970	100.0	374	5 PCT-US95-0476-2	Sequence 2, Appli
6	1970	100.0	387	4 US-09-949-016-11222	Sequence 11222, A
7	1823	92.5	344	3 US-08-466-343D-9	Sequence 9, Appli
8	1823	92.5	344	4 US-09-502-784A-9	Sequence 9, Appli
9	1727.5	87.7	329	4 US-09-783A-9	Sequence 9, Appli
10	1727.5	87.7	329	4 US-09-339-912A-9	Sequence 9, Appli
11	1727.5	87.7	329	4 US-09-195-662A-9	Sequence 9, Appli
12	1651.5	83.8	360	1 US-08-450-393A-4	Sequence 4, Appli
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14	1651.5	83.8	360	3 US-09-045-583-50	Sequence 50, Appli
15	1651.5	83.8	360	4 US-09-534-185-50	Sequence 50, Appli
16	1651.5	83.8	360	4 US-09-131-827A-2	Sequence 50, Appli
17	1651.5	83.8	360	4 US-09-625-573-4	Sequence 4, Appli
18	1651.5	83.8	360	5 PCT-US95-0476-4	Sequence 4, Appli
19	1651.5	83.8	377	4 US-09-949-016-11221	Sequence 11221, A
20	1650.5	83.8	360	4 US-09-131-827A-20	Sequence 20, Appli
21	1645.5	83.5	360	4 US-08-833-752-7	Sequence 7, Appli
22	1645.5	83.5	360	4 US-09-938-719-7	Sequence 7, Appli
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24	1645.5	83.5	360	4 US-09-826-509-473	Sequence 473, Appli
25	1614.5	82.0	360	4 US-09-045-583-51	Sequence 51, Appli
26	1614.5	82.0	360	4 US-09-534-185-51	Sequence 51, Appli
27	1589.5	80.7	347	1 US-08-461-244-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-450-393A-2
; Sequence 2, Application US/08450393A
; Patent No. 5707415

GENERAL INFORMATION:

APPLICANT: Charo, Israel

APPLICANT: Coughlin, Shaun

TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

STREET: 5 Palo Alto Square

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94306-2155

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,393A

FILING DATE: May 25, 1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Cser, Luann

REGISTRATION NUMBER: 31,822

REFERENCE/DOCKET NUMBER: UCAL-237/02US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-843-5165

TELEFAX: 415-885-0663

TELELEX: 388816coolbypa

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 374 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-450-393A-2

Query Match

Best Local Similarity

Matches 374;

Conservative 0;

Indels 0;

Gaps 0;

Query Score 100.0%;

DB 1%; Length 374;

Pred. No. 4.3e-150;

Mismatches 0;

Indels 0;

Gaps 0;

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1 MLSTSRSRIRNTNEGEEVTFFDYDYGAPCKFDVRQIGAQLPPLYSVTFGFVGN 60

82.0

360 4 US-09-826-509-473

Sequence 51, Appli

Sequence 51, Appli

Sequence 3, Appli

1 MLSTSRSRIRNTNNGEVTFFDIDYGAPECHKFDYKQIGQLLPLSVPFIFGVGN 60

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Qy 121 HIGYFGGIFFILLTDRYLAIHVAFALKARTVTFGVTSVITWLVAFAVFSVPGIIFTK 180

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Db 301 NPIIYAFGEKFRSLFHIALGCRIAPIQPKVCGGPYVRPGKKNVKTQGLLDRGKGKSI 360

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Db 361 GRAPEASLQDEGA 374

Qy 361 GRAPEASLQDEGA 374

Db 361 GRAPEASLQDEGA 374

RESULT 2
US-046-669-2
; Sequence 2, Application US/08446669
; Patent No. 6132987

GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446, 669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neely, Richard
; REGISTRATION NUMBER: 30,092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEX: 380816COOLYPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match 100 %; Score 1970; DB 3; Length 374;
Best Local Similarity 100 %; Pred. No. 4.3e-150; Indels 0; Gaps 0;

Qy 1 MLSTSRSRIRNTNNGEVTFFDIDYGAPECHKFDYKQIGQLLPLSVPFIFGVGN 60

Db 1 MLVVVLLINCKLKCLKDYLNLNAISDLFLITLPLWAHSAAANEWFGNAMCKLFITGLY 120

Qy 121 HIGYFGGIFFILLTDRYLAIHVAFALKARTVTFGVTSVITWLVAFAVFSVPGIIFTK 180

Db 121 HIGYFGGIFFILLTDRYLAIHVAFALKARTVTFGVTSVITWLVAFAVFSVPGIIFTK 180

Qy 181 CQKEDSYVCCGPYFPGRWNFTIMRNLGLVPLLMIVCYSGILKTLLRCNEKGHR 240

Db 181 CQKEDSYVCCGPYFPGRWNFTIMRNLGLVPLLMIVCYSGILKTLLRCNEKGHR 240

Qy 241 AVRIFTIMIVYFLFWTPYNVTLNNTQEFFLSNCESTSOLDQATOYTETLGMTHCCI 300

Db 241 AVRIFTIMIVYFLFWTPYNVTLNNTQEFFLSNCESTSOLDQATOYTETLGMTHCCI 300

Qy 301 NPIIYAFGEKFRSLFHIALGCRIAPIQPKVCGGPYVRPGKKNVKTQGLLDRGKGKSI 360

Db 301 NPIIYAFGEKFRSLFHIALGCRIAPIQPKVCGGPYVRPGKKNVKTQGLLDRGKGKSI 360

Qy 361 GRAPEASLQDEGA 374

Db 361 GRAPEASLQDEGA 374

RESULT 3
US-10-039-659A-14
; sequence 14, Application US/10039659A
; Patent No. 6723520

GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Vicari, Alain P.
; TITLE OF INVENTION: Antibodies that bind chemokine TACK
; CURRENT APPLICATION NUMBER: US/10/039,659A
; CURRENT FILING DATE: 2002-01-03
; PRIORITY NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIORITY NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIORITY NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIORITY NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100 %; Score 1970; DB 4; Length 374;
Best Local Similarity 100 %; Pred. No. 4.3e-150; Indels 0; Gaps 0;

Qy 1 MLSTSRSRIRNTNNGEVTFFDIDYGAPECHKFDYKQIGQLLPLSVPFIFGVGN 60

Db 1 MLVVVLLINCKLKCLKDYLNLNAISDLFLITLPLWAHSAAANEWFGNAMCKLFITGLY 120

RESULT 4

Qy	181 CQEDESVVYCGPPRGNNNFTIMRNILGLVPLIMIVCYSGILKTLRLCRNEKKHR	240	Db	61 MLVYLILINCKKLKCLTDIYLNLAISDLFLITLPLWAHSAANNEWVFGNAMCKLFITGLY	120
Db	181 CQEDESVVYCGPPRGNNNFTIMRNILGLVPLIMIVCYSGILKTLRLCRNEKKHR	240	Qy	121 HIGYFGGIPFILLTIDRYLAIVEAPALKARTVTPGVTTSVITWLAVFASVPGIIFTK	180
Qy	241 AYRIFTIMIVYFLWTPNIVLNTFOBFFGLSNCESTSQLDQATOVTETLGMTMCCI	300	Db	121 HIGYFGGIPFILLTIDRYLAIVEAPALKARTVTPGVTTSVITWLAVFASVPGIIFTK	180
Db	241 AYRIFTIMIVYFLWTPNIVLNTFOBFFGLSNCESTSQLDQATOVTETLGMTMCCI	300	Qy	181 CQEDESVVYCGPPGRNNFTIMRNILGLVPLIMIVCYSGILKTLRLCRNEKKHR	240
Qy	301 NPIIYAFGEKFRSLFHIALGCRATPLQPVCGPGRKVNKVTTQCLLDRGKGS1	360	Db	181 CQEDESVVYCGPPGRNNFTIMRNILGLVPLIMIVCYSGILKTLRLCRNEKKHR	240
Db	301 NPIIYAFGEKFRSLFHIALGCRATPLQPVCGPGRKVNKVTTQCLLDRGKGS1	360	Qy	241 AYRIFTIMIVYFLWTPNIVLNTFOBFFGLSNCESTSQLDQATOVTETLGMTMCCI	300
Qy	361 GRAPPASLQDKEGA 374		Db	241 AYRIFTIMIVYFLWTPNIVLNTFOBFFGLSNCESTSQLDQATOVTETLGMTMCCI	300
Db	361 GRAPPASLQDKEGA 374		Qy	301 NPIIYAFGEKFRSLFHIALGCRATPLQPVCGPGRKVNKVTTQCLLDRGKGS1	360
Db	361 GRAPPASLQDKEGA 374		Db	301 NPIIYAFGEKFRSLFHIALGCRATPLQPVCGPGRKVNKVTTQCLLDRGKGS1	360

RESULT 5

;	Sequence 2, Application US/09625573	PCT-US95-00476-2
;	Patent No. 6730001	; Sequence 2, Application PC/TUS9500476
;	GENERAL INFORMATION:	; GENERAL INFORMATION:
;	APPLICANT: Charo, Israel	; APPLICANT: The Regents of the University of California
;	Coughlin, Shaun	; ADDRESS: MAMMALIAN MONOCYTE CHEMOATTRACTANT
;	NUMBER OF SEQUENCES: 14	; TITLE OF INVENTION: PROTEIN RECEPTORS
;	CORRESPONDENCE ADDRESS:	; NUMBER OF SEQUENCES: 14
;	ADDRESSEER: Cooley Godward Castro Huddleston & Tatum	; CORRESPONDENCE ADDRESS: Robbins, Berliner & Carbon
;	STREET: 5 Palo Alto Square	; STREET: 201 N. Figueroa Street, 5th Floor
;	CITY: Palo Alto	; CITY: Los Angeles
;	STATE: California	; STATE: California
;	COUNTRY: USA	; COUNTRY: USA
;	ZIP: 94306-2155	; ZIP: 90012-2628
;	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:
;	MEDIUM TYPE: Floppy disk	MEDIUM TYPE: Floppy disk
;	COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible
;	OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS
;	SOFTWARE: PatentIn Release #1.0, Version #1.25	SOFTWARE: Patenter Release #1.0, Version #1.25
;	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:
;	APPLICATION NUMBER: US/09/625,573	APPLICATION NUMBER: US/09/625,573
;	FILING DATE: 25-Jul-2000	FILING DATE: 25-Jul-2000
;	CLASSIFICATION: <Unknown>	CLASSIFICATION: <Unknown>
;	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:
;	APPLICATION NUMBER: US/08/446,669 .	APPLICATION NUMBER: US/08/446,669 .
;	FILING DATE: May 25, 1995	FILING DATE: May 25, 1995
;	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:
;	NAME: Neely, Richard	NAME: Berliner, Robert
;	REGISTRATION NUMBER: 30,092	REGISTRATION NUMBER: 20,121
;	REFERENCE/DOCKET NUMBER: UCAL-237/01US	REFERENCE/DOCKET NUMBER: 5555-291
;	TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:
;	TELEPHONE: 415-843-5000	TELEPHONE: 310-977-1001
;	TELEFAX: 415-857-0663	TELEFAX: 310-977-1003
;	TELEX: 360816cooleyPA	TELEX:
;	INFORMATION FOR SEQ ID NO: 2:	INFORMATION FOR SEQ ID NO: 2:
;	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:
;	LENGTH: 374 amino acids	LENGTH: 374 amino acids
;	TYPE: amino acid	TYPE: amino acid
;	TOPOLogy: linear	TOPOLogy: linear
;	MOLECULE TYPE: protein	MOLECULE TYPE: protein
;	SEQUENCE DESCRIPTION: SEQ ID NO: 2:	SEQUENCE DESCRIPTION: SEQ ID NO: 2:
;	US-09-625-573-2	PCT-US95-00476-2

Query Match Score 100.0%; Score 1970; DB 5; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.3e-150; Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MLSTSRSRTRNTNESGREVTTFDYDGAFCPKFDVQIGAQOLPLPLSLYVTFGFVGN	60	Qy	1 MLSTSRSRTRNTNESGREVTTFDYDGAFCPKFDVQIGAQOLPLPLSLYVTFGFVGN	60
Db	1 MLSTSRSRTRNTNESGREVTTFDYDGAFCPKFDVQIGAQOLPLPLSLYVTFGFVGN	60	Db	1 MLSTSRSRTRNTNESGREVTTFDYDGAFCPKFDVQIGAQOLPLPLSLYVTFGFVGN	60
Qy	61 MLVYLILINCKKLKCLTDIYLNLAISDLFLITLPLWAHSAANNEWVFGNAMCKLFITGLY	120	Qy	61 MLVYLILINCKKLKCLTDIYLNLAISDLFLITLPLWAHSAANNEWVFGNAMCKLFITGLY	120

RESULT 8
 US-09-502-783A-9

Query Match 87.7%; Score 1727.5; DB 4; Length 329;
 Best Local Similarity 95.6%; Pred. No. 9.0e-131;
 Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

TYPE: PRT
 ORGANISM: Protein
 US-09-502-783A-9

GENERAL INFORMATION:
 APPLICANT: Li, Yi
 APPLICANT: Ruben, Steven M.
 TITLE OF INVENTION: Methods of Screening Using Human G-Protein Receptor HGDRN10 (CCRS)
 FILE REFERENCE: 1488.1150005
 CURRENT APPLICATION NUMBER: US/09/502,784A
 CURRENT FILING DATE: 2000-02-11
 PRIOR APPLICATION NUMBER: 09/195,662
 PRIOR FILING DATE: 1998-11-18
 PRIOR APPLICATION NUMBER: 08/466,343
 PRIOR FILING DATE: 1995-06-06
 SOFTWARE: PatentIn Version 3.1
 SEQ ID NO 9
 LENGTH: 344
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-09-502-783A-9

Query Match 92.5%; Score 1823; DB 4; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2.3e-118;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 78 DIVINNLAISDLIFLITPLWAHSAANWFGNAMCKLFTGLHYGGIFFLITID 137
 Db 61 DIVINNLAISDLIFLITPLWAHSAANWFGNAMCKLFTGLHYGGIFFLITID 120
 Query Match 138 RYLAIVHAFALKARTVFGVTSVITLAVAPASVPGIFTKQKEQDSVYVCGPYPRG 197
 Db 121 RYLAIVHAFALKARTVFGVTSVITLAVAPASVPGIFTKQKEQDSVYVCGPYPRG 180
 Query Match 78 DIVINNLAISDLIFLITPLWAHSAANWFGNAMCKLFTGLHYGGIFFLITID 137
 Db 61 DIVINNLAISDLIFLITPLWAHSAANWFGNAMCKLFTGLHYGGIFFLITID 105
 Query Match 138 RYLAIVHAFALKARTVFGVTSVITLAVAPASVPGIFTKQKEQDSVYVCGPYPRG 197
 Db 106 RYLAIVHAFALKARTVFGVTSVITLAVAPASVPGIFTKQKEQDSVYVCGPYPRG 165
 Query Match 78 DIVINNLAISDLIFLITPLWAHSAANWFGNAMCKLFTGLHYGGIFFLITID 137
 Db 61 DIVINNLAISDLIFLITPLWAHSAANWFGNAMCKLFTGLHYGGIFFLITID 105
 Query Match 138 RYLAIVHAFALKARTVFGVTSVITLAVAPASVPGIFTKQKEQDSVYVCGPYPRG 197
 Db 106 RYLAIVHAFALKARTVFGVTSVITLAVAPASVPGIFTKQKEQDSVYVCGPYPRG 165
 Query Match 78 DIVINNLAISDLIFLITPLWAHSAANWFGNAMCKLFTGLHYGGIFFLITID 137
 Db 61 DIVINNLAISDLIFLITPLWAHSAANWFGNAMCKLFTGLHYGGIFFLITID 105
 Query Match 138 RYLAIVHAFALKARTVFGVTSVITLAVAPASVPGIFTKQKEQDSVYVCGPYPRG 197

RESULT 9
 US-09-502-783A-9

Query Match 87.7%; Score 1727.5; DB 4; Length 329;
 Best Local Similarity 95.6%; Pred. No. 9.0e-131;
 Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

TYPE: PRT
 ORGANISM: Protein
 US-09-502-783A-9

GENERAL INFORMATION:
 APPLICANT: Li, Yi
 APPLICANT: Ruben, Steven M.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
 FILE REFERENCE: 1488.1150006
 CURRENT APPLICATION NUMBER: US/09/502,783A
 CURRENT FILING DATE: 2001-08-23
 PRIOR APPLICATION NUMBER: 08/466,343
 PRIOR FILING DATE: 1995-06-06
 NUMBER OF SEQ ID NOS: 9

Query Match 78 DIVINNLAISDLIFLITPLWAHSAANWFGNAMCKLFTGLHYGGIFFLITID 137
 Db 61 DIVINNLAISDLIFLITPLWAHSAANWFGNAMCKLFTGLHYGGIFFLITID 105
 Query Match 138 RYLAIVHAFALKARTVFGVTSVITLAVAPASVPGIFTKQKEQDSVYVCGPYPRG 197

Page 6

NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooley Godward Castro Huddleston & Tatum
 STREET: 5 Palo Alto Square
 CITY: Palo Alto
 STATE: California
 ZIP: 94306-2155
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/446,669
 FILING DATE: May 25, 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Neeley, Richard
 REGISTRATION NUMBER: 30,092
 REFERENCE/DOCKET NUMBER: UCAL-237/01US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-5000
 TELEFAX: 415-857-0663
 TELEX: 380816COOLEYPA
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 360 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-446-669-4

Query Match Score 1651.5; DB 3; Length 360;

Best Local Similarity 95.5%; Pred. No. 1.3e-124;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSRTRNTNESGEETVTFDDYDGA^PCKH^KFDVQIGAQOLPPLYSVPIFGFVN 60
 Db 1 MLSTSRSRTRNTNESGEETVTFDDYDGA^PCKH^KFDVQIGAQOLPPLYSVPIFGFVN 60
 Qy 61 MLVVLILINCKKLKCLTDIYLNLAIISDLFLITLPLWAHSAAANEWFGNAMCKLFITGLY 120
 Db 61 MLVVLILINCKKLKCLTDIYLNLAIISDLFLITLPLWAHSAAANEWFGNAMCKLFITGLY 120
 Qy 121 HIGYFGGIPFILLTIDRYLA^THAVFALKARTVPGVTSVITWLAVFASVPGIIFTK 180
 Db 121 HIGYFGGIPFILLTIDRYLA^THAVFALKARTVPGVTSVITWLAVFASVPGIIFTK 180
 Qy 181 CQKBDSTVCGPF^ILLTIDRYLA^THAVFALKARTVPGVTSVITWLAVFASVPGIIFTK 180
 Db 181 CQKBDSTVCGPF^ILLTIDRYLA^THAVFALKARTVPGVTSVITWLAVFASVPGIIFTK 180
 Qy 181 CQEDSVYVGPyPRGMNNFHMTMRNLLGVLPLLTIVLYCYSGILKTLLRCNEKGRHR 240
 Db 181 CQEDSVYVGPyPRGMNNFHMTMRNLLGVLPLLTIVLYCYSGILKTLLRCNEKGRHR 240
 Qy 241 AYRVTFTIMIVYFLFWTPNIVLNTQFFGNSNCESTS^SQDQATQVETLGMTMCC1 300
 Db 241 AYRVTFTIMIVYFLFWTPNIVLNTQFFGNSNCESTS^SQDQATQVETLGMTMCC1 300
 Qy 301 NPIIYAFGEKFR--SLF---HIALG-CRIAPL 327
 Db 301 NPIIYAFGEKFRRLSVFPRKHITKRFCKQCPV 334

RESULT 14

US-09-045-583-50
 Sequence 50, Application US/09045583
 Patent No. 628705
 GENERAL INFORMATION:
 APPLICANT: Graham, Gerard J. et al.
 TITLE OF INVENTION: No. 628705 Molecules of the G Protein-Coupled
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street

RESULT 15

US-09-534-165-50
 Sequence 50, Application US/09534185
 Patent No. 6403767
 GENERAL INFORMATION:
 APPLICANT: Graham, Gerard J. et al.
 TITLE OF INVENTION: No. 6403767 Molecules of the G Protein-Coupled
 Peptahelial Receptor Superfamily and Uses
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP

Page 8

STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/534,185
 FILING DATE: 24-Mar-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/045,583
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragours, Amy E.
 REGISTRATION NUMBER: 36,207
 REREFERENCE DOCKET NUMBER: MINI-044
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 360 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 SEQDB DESCRIPTION: SEQ ID NO: 50:
 -09-534-185-50

Query Match Score 1651.5; DB 4; Length 83.8%
 Best Local Similarity 95.5%; Pred. No. 1.3e-124;
 Matches 319; Conservative 3; Mismatches 5; Indels 1

1 MLSTSRSPRIRNTNESSGEEVTFDDYGAQCKFDKQIGAQLPP
 1 MLSTSRSPRIRNTNESSGEEVTFDDYGAQCKFDKQIGAQLPP
 1 MLVYLILINCKLKLTDIVYLNLISDLPLITLPIWAHSANENT
 1 MLVYLILINCKLKLTDIVYLNLISDLPLITLPIWAHSANENT
 1 HIGFGGIFFTILLIDRYLAIVHAYFALKARTVTGFVTSVITWV
 1 HIGFGGIFFTILLIDRYLAIVHAYFALKARTVTGFVTSVITWV
 1 COKEDSVYCGPYFPRGMNNFTHTMNLGLVPLJLIMIVCYSGILM
 1 COKEDSVYCGPYFPRGMNNFTHTMNLGLVPLJLIMIVCYSGILM
 1 AYRIFTIMIVYFLFWTPYNIVLINTFQEPFGLSNCESTSOOLDAT
 1 AYRIFTIMIVYFLFWTPYNIVLINTFQEPFGLSNCESTSOOLDAT
 1 NPLIYAFGEKFR ---SLF---HIALG-CRIAPL 327

Result No.	Score	Query Match	Length	DB ID	Description
1	1970	100.0	374	10 US-09-893-512-13	Sequence 13, Appli
2	1970	100.0	374	14 US-10-039-659-14	Sequence 14, Appli
3	1970	100.0	374	14 US-10-239-422-63	Sequence 63, Appli
4	1970	100.0	374	16 US-10-754-071-14	Sequence 14, Appli
5	1970	100.0	374	16 US-10-741-601-287	Sequence 287, Appli
6	1970	100.0	374	16 US-10-791-592-2	Sequence 2, Appli
7	1970	100.0	374	16 US-10-791-166-2	Sequence 2, Appli
8	1970	100.0	374	17 US-10-759-861-14	Sequence 14, Appli
9	1970	100.0	374	17 US-10-799-736-13	Sequence 13, Appli
10	1823	92.5	344	9 US-09-779-879A-9	Sequence 9, Appli
11	1823	92.5	344	9 US-09-779-880A-9	Sequence 9, Appli
12	1823	92.5	344	14 US-10-232-686-9	Sequence 9, Appli
13	1823	92.5	344	14 US-10-067-800-9	Sequence 9, Appli
14	1823	92.5	344	14 US-10-335-833-9	Sequence 9, Appli
15	1727.5	87.7	329	9 US-09-725-285-9	Sequence 9, Appli
16	1727.5	87.7	329	9 US-09-195-662A-9	Sequence 9, Appli
17	1727.5	87.7	329	9 US-09-333-912A-9	Sequence 9, Appli
18	1727.5	87.7	329	9 US-09-502-783A-9	Sequence 9, Appli
19	1727.5	87.7	329	16 US-10-791-905-9	Sequence 9, Appli
20	1651.5	83.8	360	9 US-09-131-827A-2	Sequence 2, Appli
21	1651.5	83.8	360	14 US-10-225-567A-460	Sequence 460, Appli
22	1651.5	83.8	360	14 US-10-591-592-4	Sequence 50, Appli
23	1651.5	83.8	360	14 US-10-239-422-64	Sequence 6, Appli
24	1651.5	83.8	360	14 US-10-319-845-8	Sequence 8, Appli
25	1651.5	83.8	360	16 US-10-741-601-285	Sequence 285, Appli
26	1651.5	83.8	360	16 US-10-741-601-286	Sequence 266, Appli
27	1651.5	83.8	360	16 US-10-791-649-50	Sequence 4, Appli
28	1651.5	83.8	360	16 US-10-791-166-4	Sequence 6, Appli
29	1651.5	83.8	360	16 US-10-700-313-8	Sequence 8, Appli
30	1651.5	83.8	360	17 US-10-386-471-4	Sequence 4, Appli
31	1651.5	83.8	360	17 US-10-246-185-8	Sequence 8, Appli
32	1650.5	83.8	360	9 US-09-131-827A-20	Sequence 20, Appli
33	1645.5	83.5	360	9 US-09-719-719-7	Sequence 7, Appli
34	1645.5	83.5	360	9 US-09-939-226-7	Sequence 7, Appli
35	1645.5	83.5	360	9 US-09-938-703-7	Sequence 7, Appli
36	1645.5	83.5	360	10 US-09-326-503-473	Sequence 7, Appli
37	1645.5	83.5	360	16 US-10-661-798-7	Sequence 7, Appli
38	1645.5	83.5	360	16 US-10-612-791-7	Sequence 7, Appli
39	1645.5	83.5	360	17 US-10-225-095-473	Sequence 473, Appli
40	1614.5	82.0	360	14 US-10-64-649-51	Sequence 51, Appli
41	1589.5	80.7	347	9 US-09-114-792-3	Sequence 3, Appli
42	1589.5	80.7	347	14 US-10-176-078-3	Sequence 3, Appli
43	1589.5	80.7	347	16 US-10-993-996-3	Sequence 3, Appli
44	1582.5	80.3	384	10 US-09-093-512-14	Sequence 14, Appli
45	1582.5	80.3	384	17 US-10-799-736-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-09-893-512-13
; Sequence 13, Application US/09893512
; Publication No. US20030017530A1
; GENERAL INFORMATION:
; APPLICANT: OMNAN, CHRISTER
; TITLE OF INVENTION: RECEPTOR AND ITS USE AS LEUKOTRIENE B4
; FILE REFERENCE: 07675.001-03 SEQUENCE LISTING
; CURRENT FILING DATE: 2001-06-29
; PRIORITY APPLICATION NUMBER: 60/061,789
; PRIORITY FILING DATE: 1997-10-14
; PRIORITY APPLICATION NUMBER: 60/081,958
; PRIORITY FILING DATE: 1998-04-15
; PRIORITY APPLICATION NUMBER: 09/170,069
; PRIORITY FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 13
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-512-13

% Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1970	100.0	374	10 US-09-893-512-13	Sequence 13, Appli
2	1970	100.0	374	14 US-10-039-659-14	Sequence 14, Appli
3	1970	100.0	374	14 US-10-239-422-63	Sequence 63, Appli
4	1970	100.0	374	16 US-10-754-071-14	Sequence 14, Appli
5	1970	100.0	374	16 US-10-741-601-287	Sequence 287, Appli
6	1970	100.0	374	16 US-10-791-592-2	Sequence 2, Appli
7	1970	100.0	374	16 US-10-791-166-2	Sequence 2, Appli
8	1970	100.0	374	17 US-10-759-861-14	Sequence 14, Appli
9	1970	100.0	374	17 US-10-799-736-13	Sequence 13, Appli
10	1823	92.5	344	9 US-09-779-879A-9	Sequence 9, Appli
11	1823	92.5	344	9 US-09-779-880A-9	Sequence 9, Appli

1 MUSTSRSPRIRNTNESBEVTFFDYGAPCKFDVQIGAQQLPPOLYSLVIFGVGN 60
1 MUSTRSRSPRIRNTNESBEVTFFDYGAPCKFDVQIGAQQLPPOLYSLVIFGVGN 60
1 MUSTRSRSPRIRNTNESBEVTFFDYGAPCKFDVQIGAQQLPPOLYSLVIFGVGN 60
1 MUSTRSRSPRIRNTNESBEVTFFDYGAPCKFDVQIGAQQLPPOLYSLVIFGVGN 60
1 MLVVLILINCKLKCLTDIYLNLATSDLFLITPLWAHSANNEWFGNAMCKLFGLY 120

REMARKS: ;
 Db 61 MLVVLILNCKKLKCCLTDYLINLAISDLFLITLPIWAHSANNEWFGNANCKLFLPTGLY 120
 Qy 121 HIGYGGIPPIIPLTIDRYLAIVHAPALKARTVTFGVTSITWLVAVASVPGIIFTK 180
 Db 121 HIGYGGIPPIIPLTIDRYLAIVHAPALKARTVTFGVTSITWLVAVASVPGIIFTK 180
 Qy 181 CQEDSVTVCGYPFPRGNNFHTIMRNLTGVLPLIMIVCYSGILKTLRNECKERHR 240
 Db 181 CQEDSVTVCGPFFPRGNNFHTIMRNLTGVLPLIMIVCYSGILKTLRNECKERHR 240
 Qy 241 AYRVFTIMIVYLFWTPNIVLNTQEFFGSNCESTSOLDQATOVTETLGMTHCCI 300
 Db 241 AYRVFTIMIVYLFWTPNIVLNTQEFFGSNCESTSOLDQATOVTETLGMTHCCI 300
 Qy 301 NPIIYAFGEKFRSLFHIALGCRIAPIQKPVCGPGRPKVNVKUTTGLLDGRGKKS1 360
 Db 301 NPIIYAFGEKFRSLFHIALGCRIAPIQKPVCGPGRPKVNVKUTTGLLDGRGKKS1 360
 Qy 361 GRAPEASLQDKEGA 374
 Db 361 GRAPEASLQDKEGA 374

RESULT 2
 US-10-039-659-14
 ; Sequence 14, Application US/10039659
 Publication No. US20030018167A1

APPLICANT: Wang, Wei
 Gish, Kurt C.
 Schall, Thomas J.

Vicari, Alain P.
 Zlotnik, Albert

TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/039,659
 FILING DATE: 03-Jan-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/887,977

FILING DATE: 03-JUL-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0589KL

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-496-1992

TELEFAX: 650-496-1200

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 374 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 US-10-039-659-14

Query Match 100.0%; Score 1970; DB 14; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.4e-163;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MUSTSRSRFIRNTNESSEBVFDDYGAFCHKFDVKQIGQQLPPLYSLVFIPTGVN 60
 Db 1 MUSTSRSRFIRNTNESSEBVFDDYGAFCHKFDVKQIGQQLPPLYSLVFIPTGVN 60
 Qy 61 MLVVLILNCKKLKCCLTDYLINLAISDLFLITLPIWAHSANNEWFGNANCKLFLPTGLY 120
 Db 61 MLVVLILNCKKLKCCLTDYLINLAISDLFLITLPIWAHSANNEWFGNANCKLFLPTGLY 120
 Qy 61 HIGYFGGIPPIIPLTIDRYLAIVHAPALKARTVTFGVTSITWLVAVASVPGIIFTK 180
 Db 61 HIGYFGGIPPIIPLTIDRYLAIVHAPALKARTVTFGVTSITWLVAVASVPGIIFTK 180
 Qy 181 CQEDSVTVCGYPFPRGNNFHTIMRNLTGVLPLIMIVCYSGILKTLRNECKERHR 240
 Db 181 CQEDSVTVCGPFFPRGNNFHTIMRNLTGVLPLIMIVCYSGILKTLRNECKERHR 240
 Qy 241 AYRVFTIMIVYLFWTPNIVLNTQEFFGSNCESTSOLDQATOVTETLGMTHCCI 300
 Db 241 AYRVFTIMIVYLFWTPNIVLNTQEFFGSNCESTSOLDQATOVTETLGMTHCCI 300
 Qy 241 AVRVFTIMIVYLFWTPNIVLNTQEFFGSNCESTSOLDQATOVTETLGMTHCCI 300
 Db 241 AVRVFTIMIVYLFWTPNIVLNTQEFFGSNCESTSOLDQATOVTETLGMTHCCI 300
 Qy 301 NPIIYAFGEKFRSLFHIALGCRIAPIQKPVCGPGRPKVNVKUTTGLLDGRGKKS1 360
 Db 301 NPIIYAFGEKFRSLFHIALGCRIAPIQKPVCGPGRPKVNVKUTTGLLDGRGKKS1 360
 Qy 361 GRAPEASLQDKEGA 374
 Db 361 GRAPEASLQDKEGA 374

RESULT 3
 US-10-239-423-63
 ; Sequence 63, Application US/10239423
 ; Publication No. US2003018688A1
 GENERAL INFORMATION:
 ; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
 ; APPLICANT: HEITLAND, Aleksandra; SPONSBERG, Nikolaj
 TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
 Cell Surface Proteome of Tumor and Inflammation Cells and
 For Treating Tumor Diseases and Inflammatory Diseases,
 Preferably with the Aid of Specific Chemokine Receptor Analysis and Chemokine Receptor/Ligand Interaction
 FILE REFERENCE: 02217US
 CURRENT APPLICATION NUMBER: US/10/239,423
 CURRENT FILING DATE: 2002-09-23
 PRIORITY NUMBER: DE10016013.1
 PRIORITY NUMBER: DE10016013.1
 PRIORITY FILING DATE: 2000-03-31
 NUMBER OF SEQ ID NOS: 84
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 63
 LENGTH: 374
 TYPE: PCT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:
 OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
 US-10-239-423-63

Query Match 100.0%; Score 1970; DB 14; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.4e-163;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MUSTSRSRFIRNTNESSEBVFDDYGAFCHKFDVKQIGQQLPPLYSLVFIPTGVN 60
 Db 1 MUSTSRSRFIRNTNESSEBVFDDYGAFCHKFDVKQIGQQLPPLYSLVFIPTGVN 60
 Qy 61 MLVVLILNCKKLKCCLTDYLINLAISDLFLITLPIWAHSANNEWFGNANCKLFLPTGLY 120

APPLICANT: Charo, Israel
 Coughlin, Shaun
 TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT PROTEIN RECEPTORS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooley Godward Castro Huddleston & Tatum
 STREET: 5 Palo Alto Square
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94306-2155

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/791,592
 FILING DATE: 01-Mar-2004
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/625,573
 FILING DATE: 25-Jul-2000
 APPLICATION NUMBER: US/08/446,669
 FILING DATE: May 25, 1995

ATTORNEY/AGENT INFORMATION:
 NAME: Neely, Richard
 REGISTRATION NUMBER: 30,092
 REFERENCE/DOCKET NUMBER: UCAL-237/01US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-5000
 TELEX: 380816cooleypa
 FAX: 415-857-0663

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 374 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-791-592-2

Query Match 100.0%; Score 1970; DB 16; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3_4e-163;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRPRNTNESGEVTTFFDYDGA^PCKFDYKQIGAQQLPPLYSIVFPGVGN 60
 Db 1 MLSTSRSRPRNTNESGEVTTFFDYDGA^PCKFDYKQIGAQQLPPLYSIVFPGVGN 60

Qy 61 MLVYLILINCKLKCLDTYLLNIAISDLFLITLPLMAHSAANEVFGNAMCKLFGLY 120
 Db 61 MLVYLILINCKLKCLDTYLLNIAISDLFLITLPLWAHSAANEWVFGNAMCKLFGLY 120

Qy 121 HIGYGGIFFIILLIDRYLAIVAVFALKARTVFGVTSVITWLAVFA^SPGIIFTK 180
 Db 121 HIGYGGIFFIILLIDRYLAIVAVFALKARTVFGVTSVITWLAVFA^SPGIIFTK 180

Qy 181 CQKEDSVTYVGPFPRGMNNFTIMRNILGVLPLLIWIVCYSGILKTLRCNEKGHR 240
 Db 181 CQKEDSVTYVGPFPRGMNNFTIMRNILGVLPLLIWIVCYSGILKTLRCNEKGHR 240

Qy 241 AYRVIIFTMIVYVFELWTPVNIVLNTTFFGNSCESTSQQDQATOYTETLGMTICCI 300
 Db 241 AYRVIIFTMIVYVFELWTPVNIVLNTTFFGNSCESTSQQDQATOYTETLGMTICCI 300

Qy 301 NPIIYAFGEKFPSLHFHALGCRIAPILOPKVPGCPGPGRKANVKVTOGLDGRGKGS 1 360
 Db 301 NPIIYAFGEKFPSLHFHALGCRIAPILOPKVPGCPGPGRKANVKVTOGLDGRGKGS 1 360

Qy 361 GRAPEASLQDGEGA 374

Db 361 GRAPEASLQDGEGA 374

RESULT 7
 US-10-791-166-2
 Sequence 2, Application US/10791166
 Publication No. US20040223968A1
 ; GENERAL INFORMATION:
 APPLICANT: Charo, Israel
 Coughlin, Shaun
 TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT PROTEIN RECEPTORS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESS: Cooley Godward Castro Huddleston & Tatum
 STREET: 5 Palo Alto Square
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94306-2155
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/791,592
 FILING DATE: 01-Mar-2004
 CLASSIFICATION: <Unknown>
 PRIORITY NUMBER: US/09/625,573
 FILING DATE: May 25, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Neely, Richard
 REGISTRATION NUMBER: 30,092
 REFERENCE/DOCKET NUMBER: UCAL-237/01US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-5000
 TELEX: 380816cooleypa
 FAX: 415-857-0663
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 374 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-791-166-2

Query Match 100.0%; Score 1970; DB 16; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3_4e-163;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRPRNTNESGEVTTFFDYDGA^PCKFDYKQIGAQQLPPLYSIVFPGVGN 60
 Db 1 MLSTSRSRPRNTNESGEVTTFFDYDGA^PCKFDYKQIGAQQLPPLYSIVFPGVGN 60

Qy 61 MLVYLILINCKLKCLDTYLLNIAISDLFLITLPLMAHSAANEVFGNAMCKLFGLY 120
 Db 61 MLVYLILINCKLKCLDTYLLNIAISDLFLITLPLWAHSAANEWVFGNAMCKLFGLY 120

Qy 121 HIGYGGIFFIILLIDRYLAIVAVFALKARTVFGVTSVITWLAVFA^SPGIIFTK 180
 Db 121 HIGYGGIFFIILLIDRYLAIVAVFALKARTVFGVTSVITWLAVFA^SPGIIFTK 180

Qy 181 CQKEDSVTYVGPFPRGMNNFTIMRNILGVLPLLIWIVCYSGILKTLRCNEKGHR 240
 Db 181 CQKEDSVTYVGPFPRGMNNFTIMRNILGVLPLLIWIVCYSGILKTLRCNEKGHR 240

Qy 241 AYRVIIFTMIVYVFELWTPVNIVLNTTFFGNSCESTSQQDQATOYTETLGMTICCI 300
 Db 241 AYRVIIFTMIVYVFELWTPVNIVLNTTFFGNSCESTSQQDQATOYTETLGMTICCI 300

Qy 301 NPIIYAFGEKFPSLHFHALGCRIAPILOPKVPGCPGPGRKANVKVTOGLDGRGKGS 1 360
 Db 301 NPIIYAFGEKFPSLHFHALGCRIAPILOPKVPGCPGPGRKANVKVTOGLDGRGKGS 1 360

Qy 361 GRAPEASLQDGEGA 374

Db 361 GRAPEASLQDKEGA 374

Db 361 GRAPEASLQDKEGA 374

RESULT 9
US-10-799-736-13
; Sequence 13, Application US/10799736
; Publication No. US20050118675A1
GENERAL INFORMATION:
APPLICANT: OWMAN, CHRISTIE
TITLE OF INVENTION: HEPTAHelix RECEPTOR AND ITS USE AS LEUKOTRIENE B4
FILE REFERENCE: 07675 0001-03 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/10/799,736
PRIORITY APPLICATION NUMBER: US/09/893,512
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/240,512
PRIOR FILING DATE: 1997-10-14
PRIOR APPLICATION NUMBER: 60/061,789
APPLICANT: Gish, Kurt C.
APPLICANT: Schall, Thomas J.
APPLICANT: Vicari, Alain P.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods for using chemokine TCK
FILE REFERENCE: DX05B9KID US
CURRENT APPLICATION NUMBER: US/10/759,860
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: US 10/039,659
PRIOR FILING DATE: 2002-01-03
PRIOR APPLICATION NUMBER: US 08/887,977
PRIOR FILING DATE: 1997-07-03
PRIOR APPLICATION NUMBER: US 60/021,664
PRIOR FILING DATE: 1996-07-05
PRIOR APPLICATION NUMBER: US 60/028,329
PRIOR FILING DATE: 1996-10-11
PRIOR APPLICATION NUMBER: US 60/048,593
PRIOR FILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-799-736-13

Query Match 100.0%; Score 1970; DB 17; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLSTSRSRFRNTNNGEEVTTFFDYDGAPEKHDVKQIGAQIPLPLYSIVFTFGVGN
Db 1 MLSTSRSRFRNTNNGEEVTTFFDYDGAPEKHDVKQIGAQIPLPLYSIVFTFGVGN
Qy 1 MLVVLLINCKKLCKLTDIVLNLAISDLFLITPLWAHSANNEWFGNAMCKLFTGGLY
Qy 61 MLVVLLINCKKLCKLTDIVLNLAISDLFLITPLWAHSANNEWFGNAMCKLFTGGLY 120
Db 61 MLVVLLINCKKLCKLTDIVLNLAISDLFLITPLWAHSANNEWFGNAMCKLFTGGLY 120
Qy 121 HIGYFGIFFTILLTDRYLAIVHAFALKARTVTFGVTSVITLVAVASVPGIFTK 180
Db 121 HIGYFGIFFTILLTDRYLAIVHAFALKARTVTFGVTSVITLVAVASVPGIFTK 180
Qy 181 CQKEDSYYVCGPYFPRGMNNFTIMRNLIQVLPLIMVTCYSGIKTKLRLCRNEKVRHR 240
Db 181 CQKEDSYYVCGPYFPRGMNNFTIMRNLIQVLPLIMVTCYSGIKTKLRLCRNEKVRHR 240
Qy 241 AVRVTITIMVYFLWTPNVIILNTFOEFFGNSCESTSQLDATQTETLGTHCC1 300
Db 241 AVRVTITIMVYFLWTPNVIILNTFOEFFGNSCESTSQLDATQTETLGTHCC1 300
Qy 301 NPITYAFGEKFRSLIFHIALGCRIALPQLKEVCGFPGRPSKGNVKTTOGLDGRKGKSI 360
Db 301 NPITYAFGEKFRSLIFHIALGCRIALPQLKEVCGFPGRPSKGNVKTTOGLDGRKGKSI 360
Qy 361 GRAPEASLQDKEGA 374
Db 361 GRAPEASLQDKEGA 374

RESULT 10
US-09-779-879A-9
; Sequence 9, Application US/0979879A
; Patent No. US20020048786A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Roschke, Viktor
APPLICANT: Li, Yi Steven, M.
APPLICANT: Rubin, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10

Db 361 GRAPEASLQDKEGA 374

Db 361 GRAPEASLQDKEGA 374

RESULT 8
US-10-759-860-14
Sequence 14, Application US/10759860
Publication No. US20050074790A1
GENERAL INFORMATION:
APPLICANT: Gish, Kurt C.
APPLICANT: Schall, Thomas J.
APPLICANT: Vicari, Alain P.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods for using chemokine TCK
FILE REFERENCE: DX05B9KID US
CURRENT APPLICATION NUMBER: US/10/759,860
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: US 10/039,659
PRIOR FILING DATE: 2002-01-03
PRIOR APPLICATION NUMBER: US 08/887,977
PRIOR FILING DATE: 1997-07-03
PRIOR APPLICATION NUMBER: US 60/021,664
PRIOR FILING DATE: 1996-07-05
PRIOR APPLICATION NUMBER: US 60/028,329
PRIOR FILING DATE: 1996-10-11
PRIOR APPLICATION NUMBER: US 60/048,593
PRIOR FILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-759-860-14

Query Match 100.0%; Score 1970; DB 17; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLSTSRSRFRNTNNGEEVTTFFDYDGAPEKHDVKQIGAQIPLPLYSIVFTFGVGN 60
Db 1 MLSTSRSRFRNTNNGEEVTTFFDYDGAPEKHDVKQIGAQIPLPLYSIVFTFGVGN 60
Qy 1 MLVVLLINCKKLCKLTDIVLNLAISDLFLITPLWAHSANNEWFGNAMCKLFTGGLY
Qy 61 MLVVLLINCKKLCKLTDIVLNLAISDLFLITPLWAHSANNEWFGNAMCKLFTGGLY 120
Db 61 MLVVLLINCKKLCKLTDIVLNLAISDLFLITPLWAHSANNEWFGNAMCKLFTGGLY 120
Qy 121 HIGYFGIFFTILLTDRYLAIVHAFALKARTVTFGVTSVITLVAVASVPGIFTK 180
Db 121 HIGYFGIFFTILLTDRYLAIVHAFALKARTVTFGVTSVITLVAVASVPGIFTK 180
Qy 181 CQKEDSYYVCGPYFPRGMNNFTIMRNLIQVLPLIMVTCYSGIKTKLRLCRNEKVRHR 240
Db 181 CQKEDSYYVCGPYFPRGMNNFTIMRNLIQVLPLIMVTCYSGIKTKLRLCRNEKVRHR 240
Qy 241 AVRVTITIMVYFLWTPNVIILNTFOEFFGNSCESTSQLDATQTETLGTHCC1 300
Db 241 AVRVTITIMVYFLWTPNVIILNTFOEFFGNSCESTSQLDATQTETLGTHCC1 300
Qy 301 NPITYAFGEKFRSLIFHIALGCRIALPQLKEVCGFPGRPSKGNVKTTOGLDGRKGKSI 360
Db 301 NPITYAFGEKFRSLIFHIALGCRIALPQLKEVCGFPGRPSKGNVKTTOGLDGRKGKSI 360
Qy 361 GRAPEASLQDKEGA 374
Db 361 GRAPEASLQDKEGA 374

Db 361 GRAPEASLQDKEGA 374

Db 361 GRAPEASLQDKEGA 374

FILE REFERENCE: 1488.115000A
 CURRENT FILING DATE: US/09/779, 879A
 PRIOR APPLICATION NUMBER: US/09/779, 879A
 CURRENT FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: US 6/181, 258
 PRIOR FILING DATE: 2000-02-09
 PRIOR APPLICATION NUMBER: US 6/187, 999
 CURRENT FILING DATE: 2000-03-09
 PRIOR APPLICATION NUMBER: US 6/187, 999
 PRIOR FILING DATE: 2000-03-09
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 9
 LENGTH: 344
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-779-879A-9

Query Match 92.5%; Score 1823; DB 9; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2e-150;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EEVTTFFDYDYGAPCHKEVDVKIGAQQLPPLYSLVPFGFVNMLVYLINCKLKCLT 77
 Db 1 EEVTTFFDYDYGAPCHKEVDVKIGAQQLPPLYSLVPFGFVNMLVYLINCKLKCLT 60

Qy 78 DYLNNLAISDLFLITPLWAHSAAANEWFGNAMCQLFTGLYHIGYFGGIFPIILITID 137
 Db 61 DYLNNLAISDLFLITPLWAHSAAANEWFGNAMCQLFTGLYHIGYFGGIFPIILITID 120

Qy 138 RYLAIVHAFALKARTTFFGUTSITWLVAVASVPGIILFVKCOKEDSVVYCGPYPRG 197
 Db 121 RYLAIVHAFALKARTTFFGUTSITWLVAVASVPGIILFVKCOKEDSVVYCGPYPRG 180

Qy 138 RYLAIVHAFALKARTTFFGUTSITWLVAVASVPGIILFVKCOKEDSVVYCGPYPRG 197
 Db 121 RYLAIVHAFALKARTTFFGUTSITWLVAVASVPGIILFVKCOKEDSVVYCGPYPRG 180

Qy 198 WNNFHTIMRNLLGLVLLIMIVYCGSILKTLRCRNEKKHRRAVRVITIMIVYFELWT 257
 Db 181 WNNFHTIMRNLLGLVLLIMIVYCGSILKTLRCRNEKKHRRAVRVITIMIVYFELWT 240

Qy 258 PYNIVILLANTFOBEFGHSNCESTSQLDATOTVETLGTMTHCCINPIIYAFGEKFKRSLFH 317
 Db 241 PYNIVILLANTFOBEFGHSNCESTSQLDATOTVETLGTMTHCCINPIIYAFGEKFKRSLFH 300

Qy 318 IALGCRIAPLQPKVPGPVGPRGKAVVTVTQGLDGSGKGKSIG 361
 Db 301 IALGCRIAPLQPKVPGPVGPRGKAVVTVTQGLDGSGKGKSIG 344

RESULT 12
 US-10-232-686-9
 ; Sequence 9, Application US/10232686
 ; Publication No. US200302304A1

GENERAL INFORMATION:
 ; APPLICANT: Li, Yi
 ; INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
 ; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
 ; CURRENT APPLICATION NUMBER: US/10/232-686
 ; CURRENT FILING DATE: 2002-09-03
 ; PRIORITY: 1988-11-15 000N
 ; FILE REFERENCE: 1488.115000A
 ; PRIORITY APPLICATION NUMBER: 09/339, 912
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIORITY APPLICATION NUMBER: 09/195, 662
 ; PRIOR FILING DATE: 1998-11-18
 ; PRIORITY APPLICATION NUMBER: 08/466, 343
 ; PRIOR FILING DATE: 1995-06-06
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 9
 ; LENGTH: 344
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-232-686-9

Query Match 92.5%; Score 1823; DB 14; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2e-150;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EEVTTFFDYDYGAPCHKEVDVKIGAQQLPPLYSLVPFGFVNMLVYLINCKLKCLT 77
 Db 1 EEVTTFFDYDYGAPCHKEVDVKIGAQQLPPLYSLVPFGFVNMLVYLINCKLKCLT 60

Qy 78 DYLNNLAISDLFLITPLWAHSAAANEWFGNAMCQLFTGLYHIGYFGGIFPIILITID 137
 Db 61 DYLNNLAISDLFLITPLWAHSAAANEWFGNAMCQLFTGLYHIGYFGGIFPIILITID 120

Qy 138 RYLAIVHAFALKARTTFFGUTSITWLVAVASVPGIILFVKCOKEDSVVYCGPYPRG 197
 Db 121 RYLAIVHAFALKARTTFFGUTSITWLVAVASVPGIILFVKCOKEDSVVYCGPYPRG 180

Qy 198 WNNFHTIMRNLLGLVLLIMIVYCGSILKTLRCRNEKKHRRAVRVITIMIVYFELWT 257
 Db 181 WNNFHTIMRNLLGLVLLIMIVYCGSILKTLRCRNEKKHRRAVRVITIMIVYFELWT 240

Qy 258 PYNIVILLNTFOBPFGLSNCESTSOLDATQVTTENLGMTHCCINPIIYAFVGKPRSLFH 317
 Db 241 PYNIVILLNTFOBPFGLSNCESTSOLDATQVTTENLGMTHCCINPIIYAFVGKPRSLFH 300

Qy 318 IALGRIAPLQKPVCGPGRPGKVKVTQGLDGRGKSIG 361
 Db 301 IALGRIAPLQKPVCGPGRPGKVKVTQGLDGRGKSIG 344

RESULT 13 US-10-067-800-9
 ; Sequence 9, Application US/10135839
 ; Publication No. US20030166024A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen, Craig A.
 ; APPLICANT: Rosche, Viktor
 ; APPLICANT: Li, Yi
 ; APPLICANT: Ruben, Steven, M.
 ; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10
 ; FILE REFERENCE: 1488.115000A
 ; CURRENT APPLICATION NUMBER: US/10/135 , 839
 ; CURRENT FILING DATE: 2002-05-01
 ; PRIOR APPLICATION NUMBER: US/09/779, 879A
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/187, 999
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: US 60/234, 336
 ; PRIOR FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 9
 ; LENGTH: 344
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-135-839-9

Query Match 92.5%; Score 1823; DB 14; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2e-150;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 BEVTTFDDYDGPCKDPVQIGAQQLPLPLSLYFIFGFVNMLVLVILINCKKLKC LT 77
 Db 1 BEVTTFDDYDGPCKDPVQIGAQQLPLPLSLYFIFGFVNMLVLVILINCKKLKC LT 60

Qy 78 DYLNLNLASDLFLPLTPLWLAISAAANEVFGNAMCFLTGLTHIGFGCIFTLTLID 137
 Db 61 DYLNLNLASDLFLPLTPLWLAISAAANEVFGNAMCFLTGLTHIGFGCIFTLTLID 120

Qy 138 RYLAIVHAYFAFLKARTTFFGVVTSVITLAVFASVPLGIFTKQKEDESYYVCGPYFPRG 197
 Db 121 RYLAIVHAYFAFLKARTTFFGVVTSVITLAVFASVPLGIFTKQKEDESYYVCGPYFPRG 180

Qy 198 WNNFTHTIRNLNLGVPLLMIVCGSLKLTKLARNEEKHRRAVIFTIMITYFLFWT 257
 Db 181 WNNFTHTIRNLNLGVPLLMIVCGSLKLTKLARNEEKHRRAVIFTIMITYFLFWT 240

Qy 258 PYNIVILLNTFOBPFGLSNCESTSOLDATQVTTENLGMTHCCINPIIYAFVGKPRSLFH 317
 Db 241 PYNIVILLNTFOBPFGLSNCESTSOLDATQVTTENLGMTHCCINPIIYAFVGKPRSLFH 300

Qy 318 IALGRIAPLQKPVCGPGRPGKVKVTQGLDGRGKSIG 361
 Db 301 IALGRIAPLQKPVCGPGRPGKVKVTQGLDGRGKSIG 344

RESULT 15 US-09-725-285-9
 ; Sequence 9, Application US/09725285
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben, Steven, M.
 ; APPLICANT: Li, Yi
 ; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
 ; FILE REFERENCE: 1488.1150003
 ; CURRENT APPLICATION NUMBER: US/09/725 , 285
 ; CURRENT FILING DATE: 2000-11-29
 ; PRIOR APPLICATION NUMBER: 09/339, 912
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 09/195, 662
 ; PRIOR FILING DATE: 1998-11-18
 ; PRIOR APPLICATION NUMBER: 08/466, 343
 ; PRIOR FILING DATE: 1995-06-06
 ; NUMBER OF SEQ ID NOS: 9

RESULT 14 US-10-135-839-9

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; SOFTWARE: Patentin version 3.0
; SEQ_ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-725-285-9

Query Match Score 1727.5; DB 9; Length 329;
Best Local Similarity 95.6%; Pred. No. 4e-142;
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;
Matches 329; Conservatve 0; Mismatches 0; Indels 15; Gaps 1;

Qy   18 EEEVTFDDYDGAAPCKHPDKVQIGAQOLIPLPVLSPVPIRGFVNMLVVYLILINCKKLKCLT 77
Db    1 EEEVTFDDYDGAAPCKHPDKVQIGAQOLIPLPVLSPVPIRGFVNMLVVYLILINCKKLKCLT 60
Qy   78 DYLINLAIISDLFLITPLWAISSAANEWVFGNAMCKLPTGLYHIGYFGGIPPEILLID 137
Db    61 DYLINLAIISDLFLITPLWAISSAANEWVFGNAMCKLPTGLYH----- 105
Qy   138 RYLAIVHAFLAKARTTFFGVVTSVITLVAFAASVPGIIFTMKCQKEDSVYVCGXPFRG 197
Db   106 RYLAIVHAFLAKARTTFFGVVTSVITLVAFAASVPGIIFTMKCQKESSVYVCGYPFRG 165
Qy   198 WNNFTIMTNNLGLVPLIMIVCYSGIITKTLRCRNEKKRHRAYRVIFTIMIVYFLWT 257
Db   166 WNNFTIMTNNLGLVPLIMIVCYSGIITKTLRCRNEKKRHRAYRVIFTIMIVYFLWT 225
Qy   258 PYNIVLILNTFQEPFGLSNCESTSOLDQATQVTEFLGMTHCCINPIYAFIGEKFRSLFH 317
Db   226 PYNIVLILNTFQEPFGLSNCESTSOLDQATQVTEFLGMTHCCINPIYAFIGEKFRSLFH 285
Qy   318 IALGCRRIAPLKQPVCGGGRGRGNVKVTTGQJLDGRGKGSIG 361
Db   286 IALGCRRIAPLKQPVCGGGRGRGNVKVTTGQJLDGRGKGSIG 329

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Search completed: June 9, 2005, 17:06:37
 Job time : 106.455 secs

<p>Gencore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.</p> <p>MM protein - protein search, using BW model</p>	<p>run on: June 9, 2005, 16:27:48 ; Search time 111.826 Seconds (without alignments) 1245.097 Million cell updates/sec</p>	<p>title: US-10-791-166-4</p> <p>perfect score: 1900</p> <p>sequence: I MLSTSRSRPFRTNTNESGBEV.....DGVTSTNTPTGQEVASGL 360</p>	<p>scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5</p>	<p>searched: 2105692 seqs, 386760381 residues</p> <p>total number of hits satisfying chosen parameters: 2105692</p>
--	--	--	---	---

Post-processing: Minimum Match 0% Maximum Match 100% Tries in first 45 summaries

A_Geneseq_16Dec04 : *
1:_ GeneseqP1980s : *
2:_ GeneseqP200s : *
3:_ GeneseqP200s : *
4:_ GeneseqP2001s : *
5:_ GeneseqP2002s : *
6:_ GeneseqP2003s : *
7:_ GeneseqP2030s : *
8:_ GeneseqP2004s : *

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result	No.	Score	Query	Match	Length	DB	ID	Description
1	1	1900	100.0	360	2	AAR79166	Aar079166	Human mon
	2	1900	100.0	360	2	AAW35833	Aaw35833	Human mon
	3	1900	100.0	360	4	ARG81108	Aag81108	CCR
	4	1900	100.0	360	4	AAU0614	Aau0614	Human wil
	5	1900	100.0	360	6	ABP9725	Abp9725	Amino aci
	6	1900	100.0	360	6	ABP81987	Abp81987	Human C-C
	7	1900	100.0	360	8	ADM67225	Adm67225	Human adi
	8	1900	100.0	360	8	ADL82831	Adl82831	Human PRO
	9	1899	99.9	360	4	ARU0613	Aau07613	Human che
	10	1894	99.7	360	4	ABB55340	Abb55340	Non-endog
	11	1838	96.7	347	7	ADP5627	Adf5627	Partial h
	12	1651.5	86.9	374	2	AAR79165	Aar79165	Human mon
	13	1651.5	86.9	374	4	AAGB8107	Aag8107	Human CCR
	14	1651.5	86.9	374	6	ABU0083	Abu0083	Human che
	15	1651.5	86.9	374	7	ADD44861	Add44861	Human Pro
	16	1651.5	86.9	374	7	ADD44865	Add44865	Human Pro
	17	1651.5	86.9	374	7	ADP56146	Adp56146	Human che
	18	1651.5	86.9	374	8	ADO21221	Ado2221	Human GPC
	19	1651.5	86.9	374	8	ADQ67847	Adq67847	Human che
	20	1568.5	82.6	344	5	ABGG9881	Abg92881	Class I r
	21	1568.5	82.6	344	6	ABU06155	Abu6155	Human mon
	22	1568.5	82.6	344	7	ADF71219	Adf71219	Human G-P
	23	1568.5	82.6	344	8	ADP86217	Adp86217	Human MCP
	24	1535	80.8	373	8	ADM6724	Adm6724	Murine ad
	25	1535	80.8	373	8	ADO22222	Ado22222	Mouse GPC

26	1535	80.8	373	8	ADP74040	Murine CC	
27	1473	77.5	329	4	AB46859	Human MCP	
28	1473	77.5	329	5	ABB81055	Human MCP	
29	1473	77.5	329	8	ADR16266	Human MCP	
30	1396	73.5	354	2	ADO29228	Mouse GPC	
31	1386	72.9	354	2	Aaw54037	Mouse CC-	
	32	1386	72.9	354	7	Add44859	Rat Prote
	33	1386	72.9	354	7	Add44863	Rat Prote
	34	1371	72.2	352	4	AAG79089	Am.Ind acI
	35	1364	71.8	352	2	Aaw27407	Human CCR
	36	1364	71.8	352	2	Aaw27123	Human che
	37	1364	71.8	352	2	Aaw27125	Macaque C
	38	1364	71.8	352	2	Aaw23835	Human CC
	39	1364	71.8	352	2	Aaw88232	HIV-1 co-
	40	1364	71.8	352	4	AAG80111	Human CCR
	41	1364	71.8	352	4	Aae04321	Human che
	42	1364	71.8	352	4	Aab833354	Human CCR
	43	1364	71.8	352	4	Aab82948	Human HIV
						Aab5828	
						Abb08343	
						Aab08345	
						AAM52828	
						ABB08343	

ALIGNMENTS

RESULT 1
AAR79166

AAR79166;
25-MAR-2003 (revised)
29-DEC-1995 (First entry)

Human monocyte chemoattractant protein-1 receptor MCP-1RB.
Monocyte chemoattractant protein-1 receptor: MCR-1R; chemokine.

Homo sapiens.

Key	Location/Qualifiers
Domain	1..48 /label= extracellular
Domain	49..70 /label= transmembrane
Domain	80..700 /label= transmembrane
Domain	115..136 /label= transmembrane
Domain	154..178 /label= transmembrane
Domain	204..231 /label= transmembrane
Domain	244..268 /label= transmembrane
Domain	295..313 /label= transmembrane
Region	314..360 /label= carboxyl tail

PN	WC9519436-A1.
XX	
PD	20-JUL-1995.
XX	
PF	11-JAN-1995;
XX	95WO-US000476.
PR	13-JAN-1994;
XX	94US-010182962.
PA	(REBG) UNIV CALIFORNIA.
XX	
PI	Charo I., Coughlin S.
XX	
DR	WPTI: 1995-2618666/34

DR	N-PSDB; AQ96298.	OS	Homo sapiens.
XX	DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.	XX	
PT	PT for identifying antagonists and for treating diseases characterised by	PN	JP09238688-A.
PT	monocytic infiltrates.	XX	
XX		PD	16-SEP-1997.
PS	Claim 2; Fig 2; 84pp; English.	XX	
XX	To identify and clone new members of the chemokine receptor gene family,	PF	11-MAR-1996;
CC	degenerate oligo primers were designed corresp. to the conserved	XX	96JP-00053574.
CC	sequences R79167 in the second and R79168 in the third transmembrane	PA	(TAKE) TAKEDA CHEM IND LTD.
CC	domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the	XX	
CC	HOMSTRS Orphan receptor (Genbank Accession #M99293. The degenerate oligo	WPI	1997-506557/47.
CC	incorporating EcobI and XbaI sites at their 5' ends are Q96299 and	DR	N-PSDB; AAT96976.
CC	Q96300. Amplification of cDNA derived from MM6 cells with the primers	XX	
CC	yielded a number of PCR products. One cDNA appeared to encode a novel	PT	DNA encoding human monocyte chemoattractant protein 1 receptor - used to
CC	protein. To obtain a full-length version of this clone, a MM6 cDNA	PT	treat tumours and inflammatory, viral, infectious, allergic, diabetic and
CC	library was constructed in pPROG and probed with the PCR product. A 2.1	PT	central nervous system diseases.
CC	kb cDNA clone was obt. Analysis of additional clones in the MM6 cDNA	XX	
CC	library revealed a second sequence that was identical to the 2.1 kb cDNA	PS	Disclosure; Page 12-14; 15pp; Japanese.
CC	sequence first obt. from the 5' UTR through the putative seventh	XX	
CC	transmembrane domain but contained a different cytoplasmic tail. The	CC	The present sequence represents human monocyte chemoattractant protein 1
CC	second sequence appears to represent alternative splicing of the carboxy	CC	(MCP-1) receptor protein. The MCP-1 receptor protein and encoding DNA are
CC	-terminal tail of the MCP-1R protein. The two sequences are denoted MCP-	CC	used for the prevention and treatment of tumors and inflammatory, viral,
CC	1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-	CC	infectious, allergic, diabetic and central nervous system diseases
CC	1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.	XX	
CC	wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN	SQ	Sequence 360 AA:
XX	field.)		Query Match 100.0%; Score 1900; DB 2; Length 360;
SQ	Sequence 360 AA;		Best Local Similarity 100.0%; Pred. No. 1.9e-206; Mismatches 0; Indels 0; Gaps 0;
			Matches 360; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
Qy	MLSTSRSPRTNTNESGEEVTTFPDYDGA	Qy	MLSTSRSPRTNTNESGEEVTTFPDYDGA
Db	1 KFDVQIGAQOLLPLPLSILYPIFGFVGN	Db	1 KFDVQIGAQOLLPLPLSILYPIFGFVGN
Qy	60 60	Qy	60 60
Db	1 MLVYLILINCKKLKCLTDIYLNLAIISDLFLITLPLWAHSAANEWVGNANCKLFGLY	Db	1 MLVYLILINCKKLKCLTDIYLNLAIISDLFLITLPLWAHSAANEWVGNANCKLFGLY
Qy	61 61	Qy	61 61
Db	1 MLVYLILINCKKLKCLTDIYLNLAIISDLFLITLPLWAHSAANEWVGNANCKLFGLY	Db	1 MLVYLILINCKKLKCLTDIYLNLAIISDLFLITLPLWAHSAANEWVGNANCKLFGLY
Qy	121 HIGYFGGIFPFIILITIDRYLAIVHAVALKARTVTGFVTSVITWLAVAFASVPGIIFTK	Qy	121 HIGYFGGIFPFIILITIDRYLAIVHAVALKARTVTGFVTSVITWLAVAFASVPGIIFTK
Db	180 180	Db	180 180
Qy	181 CQEDSVTVCGPYPRGMNNFTIMRNLLGVLPLLIINVICYSGILKLTLLCRNEKRRHR	Qy	181 CQEDSVTVCGPYPRGMNNFTIMRNLLGVLPLLIINVICYSGILKLTLLCRNEKRRHR
Db	240 240	Db	240 240
Qy	181 CQEDSVTVCGPYPRGMNNFTIMRNLLGVLPLLIINVICYSGILKLTLLCRNEKRRHR	Qy	241 AVRVIFTIMIVYFLFWTPNIVILLNTFOEFFGLSNCESTSQLDQATOVTETLGMTHCII
Db	240 240	Db	241 AVRVIFTIMIVYFLFWTPNIVILLNTFOEFFGLSNCESTSQLDQATOVTETLGMTHCII
Qy	241 AVRVIFTIMIVYFLFWTPNIVILLNTFOEFFGLSNCESTSQLDQATOVTETLGMTHCII	Qy	301 NPIIYAFGEKFRRLSVPRKHITKRCQPVYRETVDGVTSNTPTSGEQEVSGL
Db	300 300	Db	301 NPIIYAFGEKFRRLSVPRKHITKRCQPVYRETVDGVTSNTPTSGEQEVSGL
Qy	301 NPIIYAFGEKFRRLSVPRKHITKRCQPVYRETVDGVTSNTPTSGEQEVSGL	Db	301 NPIIYAFGEKFRRLSVPRKHITKRCQPVYRETVDGVTSNTPTSGEQEVSGL
Db	360 360	Db	360 360
			RESULT 3
			ID AACB0108 standard; protein: 360 AA.
			XX AACB0108;
			AC AACB0108;
			XX DT 17-JAN-2002 (first entry)
			DB Human CCR2b protein.
			XX KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
			KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
			KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
			KW antiinflammatory; antidiabetic; immunosuppressive; dermatological;
			KW antirheumatic; antiarthritic.
			XX

RESULT 4

Db	241	AVRIFTIMIVYFLWTPNIVILLNTQEFFGLSNCESTSQDQATQVTETLGMTIICCI	300	Qy	181	COKEDSVTYVCGPYPFRGNNFTIMNNTLGLVPLLMVICYSGLTLLRCNEKEKCHR	240
Qy	301	NPIYAFGEKFRRLSYEFRKHTKFKQCPVYTFRTDGVTSNTNPSTGEQEVSAGL	360	Db	181	COKEDSVTYVCGPYPFRGNNFTIMNNTLGLVPLLMVICYSGLTLLRCNEKEKCHR	240
Db	301	NPIYAFGEKFRRLSYEFRKHTKFKQCPVYTFRTDGVTSNTNPSTGEQEVSAGL	360	Qy	241	AVRIFTIMIVYFLWTPNIVILLNTQEFFGLSNCESTSQDQATQVTETLGMTIICCI	300
AC				Db	241	AVRIFTIMIVYFLWTPNIVILLNTQEFFGLSNCESTSQDQATQVTETLGMTIICCI	300
XX				Qy	301	NPIYAFGEKFRRLSYEFRKHTKFKQCPVYTFRTDGVTSNTNPSTGEQEVSAGL	360
AC				Db	301	NPIYAFGEKFRRLSYEFRKHTKFKQCPVYTFRTDGVTSNTNPSTGEQEVSAGL	360
XX							
RESULT 5							
ABP97725							
ID	ABP97725	standard; protein; 360 AA.					
XX							
AC	ABP97725;						
XX							
DT	28-MAY-2003	(first entry)					
XX							
DE	Amino acid sequence of human chemokine receptor CCR2.						
XX							
KW	Human: chemokine receptor; CCR2; viral infection; surface protein;						
KW	respiratory virus infection; respiratory syncytial virus infection;						
KW	RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.						
XX							
OS	Homo sapiens.						
XX							
PN	WO2003014153-A2.						
XX							
PD	20-FEB-2003.						
XX							
PD	12-AUG-2002; 2002WO-CA001248.						
XX							
PR	10-AUG-2001; 2001US-0311088P.						
XX							
PA	(TOPI-) - TOPIGEN PHARM INC.						
XX							
P1	Renzi P, Zemzumi K;						
XX							
DR	WPI; 2003-256541/25.						
XX							
DR	DR-N-PSDB; ABZ66878.						
XX							
PT	Modulating viral infection of a cell, for treating or preventing						
PT	respiratory virus infections, bronchitis, pneumonia or asthma, by						
PT	modulating a binding interaction between a cell chemokine-receptor and a						
PT	surface protein of the virus.						
XX							
PS	Disclosure; Page 82-84; 120pp; English.						
XX							
CC	The present sequence represents human chemokine receptor CCR2. The						
CC	specification describes a method for modulating viral infection of a						
CC	cell. the method comprises modulating a binding interaction between a						
CC	cell chemokine-receptor and a surface protein of the virus. The proviso						
CC	is that the cell chemokine-receptor is not CX3CR1 and that the virus is						
CC	not HIV. The method is useful for treating or preventing respiratory						
CC	virus infection in vertebrates, more particularly respiratory syncytial						
CC	virus (RSV) infections, and related diseases, e.g. bronchiolitis,						
CC	bronchitis, pneumonia or asthma						
XX							
SQ	Sequence 360 AA;						
Query Match	100.0% Score 1900; DB 6; Length 360;						
Best Local Similarity	100.0%; Pred. No. 1, 9e-216;						
Matches	360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1 MLSTSRSRPIRNTNESGEVTTFFDYDGAPECKFDVKQIGAQOLLPPSLFIFGFVGN	60					
Db	1 MLSTSRSRPIRNTNESGEVTTFFDYDGAPECKFDVKQIGAQOLLPPSLFIFGFVGN	60					
Qy	61 MLVLVILINCKKLTDIYLNAISDLFLLTLPWAHSAAANEVFGNAMCKLFTGLY	120					
Db	61 MLVLVILINCKKLTDIYLNAISDLFLLTLPWAHSAAANEVFGNAMCKLFTGLY	120					
Qy	121 HIGYFGGIIFFIILITIDRYLAIVAVFAALKARTVTFGTVTSTVWLVAVFASVPGIFTK	180					
Db	121 HIGYFGGIIFFIILITIDRYLAIVAVFAALKARTVTFGTVTSTVWLVAVFASVPGIFTK	180					

CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42869 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX SQ Sequence 360 AA;

Query Match	100.0%	Score 1900;	DB 6;	Length 360;
Best Local Similarity	100.0%	Pred. No. 1..9e-206;		
Matches	360;	Mismatches 0;	Indels 0;	Gaps 0;

```

Qy      1 MLSTSRSPRTNTNESEBEVTTFFDYDGAPEKRFDVQIGAQOLPPPLSIVFPGVGN 60
Db      1 MLSTSRSPRINTNESEBEVTTFFDYDGAPEKRFDVQIGAQOLPPPLSIVFPGVGN 60
Qy      61 MLVVLINCKLKCLTDIYLLNIAISDLFLITLPLWAHSAANEWVGNAMCKLFGLY 120
Db      61 MLVVLINCKLKCLTDIYLLNIAISDLFLITLPLWAHSAANEWVGNAMCKLFGLY 120
Qy      121 HIGYFGGIPPIIILIDRYLAIVHAFALKARTTGFVTSVITMLVAVASVPGIIFTK 180
Db      121 HIGYFGGIPPIIILIDRYLAIVHAFALKARTTGFVTSVITMLVAVASVPGIIFTK 180
Qy      181 CQEDSVTCGPYPFRGMNNFHTMRLVPLLIMVICYSGILKTLRCRNEKGHR 240
Db      181 CQEDSVTCGPYPFRGMNNFHTMRLVPLLIMVICYSGILKTLRCRNEKGHR 240
Qy      241 AYRVTIMIVYLFWTPNIVILLNTFOEFFLSNCESTSOLDQATOVTETLGMTHCCI 300
Db      241 AYRVTIMIVYLFWTPNIVILLNTFOEFFLSNCESTSOLDQATOVTETLGMTHCCI 300
Qy      301 NPIIYAFGEKEFRLSYVPRKRITKRPCKOCVPYRBTVDGTSTNTPSTGEQEVSAGL 360
Db      301 NPIIYAFGEKEFRLSYVPRKRITKRPCKOCVPYRBTVDGTSTNTPSTGEQEVSAGL 360

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XX SQ Sequence 360 AA;

Query Match	100.0%	Score 1900;	DB 8;	Length 360;
Best Local Similarity	100.0%	Pred. No. 1..9e-206;		
Matches	360;	Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0;

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Qy      1 MLSTSRSPRINTNESEBEVTTFFDYDGAPEKRFDVQIGAQOLPPPLSIVFPGVGN 60
Db      1 MLSTSRSPRINTNESEBEVTTFFDYDGAPEKRFDVQIGAQOLPPPLSIVFPGVGN 60
Qy      61 MLVVLINCKLKCLTDIYLLNIAISDLFLITLPLWAHSAANEWVGNAMCKLFGLY 120
Db      61 MLVVLINCKLKCLTDIYLLNIAISDLFLITLPLWAHSAANEWVGNAMCKLFGLY 120
Qy      121 HIGYFGGIPPIIILIDRYLAIVHAFALKARTTGFVTSVITMLVAVASVPGIIFTK 180
Db      121 HIGYFGGIPPIIILIDRYLAIVHAFALKARTTGFVTSVITMLVAVASVPGIIFTK 180
Qy      181 CQEDSVTCGPYPFRGMNNFHTMRLVPLLIMVICYSGILKTLRCRNEKGHR 240
Db      181 CQEDSVTCGPYPFRGMNNFHTMRLVPLLIMVICYSGILKTLRCRNEKGHR 240
Qy      241 AYRVTIMIVYLFWTPNIVILLNTFOEFFLSNCESTSOLDQATOVTETLGMTHCCI 300
Db      241 AYRVTIMIVYLFWTPNIVILLNTFOEFFLSNCESTSOLDQATOVTETLGMTHCCI 300
Qy      301 NPIIYAFGEKEFRLSYVPRKRITKRPCKOCVPYRBTVDGTSTNTPSTGEQEVSAGL 360
Db      301 NPIIYAFGEKEFRLSYVPRKRITKRPCKOCVPYRBTVDGTSTNTPSTGEQEVSAGL 360

```

RESULT 7
 ADM67225 ID ADM67225 standard; protein: 360 AA.

XX AC ADL82831;
 XX DT 03-JUN-2004 (first entry)

XX Human adipocyte specific chemokine (C-C) receptor 2 protein SeqID 579.
 XX human; adipocyte specific; adipose tissue; anti-obesity;
 XX high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 XX adipogenesis; hypertension; cardiovascular disease; anorectic;
 XX antidiabetic; hypertensive; chemokine (C-C) receptor 2.
 XX Homo sapiens.
 XX WO2004011618-A2.
 XX 05-FEB-2004.

XX PP 29-JUL-2003; 2003WO-US023684.
 XX PR 12-JUN-2003; 2003US-0378206P.
 XX PA (HMGENE-) HMGENE INC.
 XX Chada K, Chouinard R, Ashar H, Sayed AMD;
 XX PI KK Immunosuppressive; Cytoplastic; Antiarthritic; Antirheumatic; Antianemic;
 XX RW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
 XX Gene Therapy; PRO; B cell related disorder; cancer;

DR WPI: 2004-143846/14.
 DR N-PSDB; ADM66946.
 XX

XX Identifying adipocyte specific genes, useful for treating obesity or diabetes, and for identifying drug targets, by differential gene expression analysis between adipose tissue or stromal vascular tissue of mice of different genotypes.
 XX Disclosure: SEQ ID NO 579; 91pp; English.

XX This invention relates to a novel method for identifying genes that are over-expressed in adipose tissue and as such it provides targets for anti-obesity pharmaceutical compositions. Specifically, it refers to a high mobility group I-C protein (HMGI-C) that is associated with obesity and is epistatic to leptin, furthermore, it refers to the ob gene where an autosomal recessive trait is linked to obesity and diabetes. The present invention describes performing differential gene expression analysis between the white adipose tissue (WAT) or stromal vascular tissue (SVT) of any two different mice selected from a group consisting of wild-type, HMGI-C +/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using this method novel nucleotides and the encoded proteins thereof were identified that are adipocyte specific, and as such can be used for preventing adipogenesis, diagnosing and treating diabetes, obesity, hypertension and cardiovascular disease, as well as screening for compounds that can modulate or prevent adipogenesis and treat diabetes or obesity. These compositions exhibit anorectic, antidiabetic and hypotensive activities. This polypeptide sequence is a human homologue of a murine adipocyte specific protein sequence of the invention.

XX SQ Sequence 360 AA;

Query Match	100.0%	Score 1900;	DB 8;	Length 360;
Best Local Similarity	100.0%	Pred. No. 1..9e-206;		
Matches	360;	Mismatches 0;	Indels 0;	Gaps 0;

```

Qy      1 MLSTSRSPRINTNESEBEVTTFFDYDGAPEKRFDVQIGAQOLPPPLSIVFPGVGN 60
Db      1 MLSTSRSPRINTNESEBEVTTFFDYDGAPEKRFDVQIGAQOLPPPLSIVFPGVGN 60
Qy      61 MLVVLINCKLKCLTDIYLLNIAISDLFLITLPLWAHSAANEWVGNAMCKLFGLY 120
Db      61 MLVVLINCKLKCLTDIYLLNIAISDLFLITLPLWAHSAANEWVGNAMCKLFGLY 120
Qy      121 HIGYFGGIPPIIILIDRYLAIVHAFALKARTTGFVTSVITMLVAVASVPGIIFTK 180
Db      121 HIGYFGGIPPIIILIDRYLAIVHAFALKARTTGFVTSVITMLVAVASVPGIIFTK 180
Qy      181 CQEDSVTCGPYPFRGMNNFHTMRLVPLLIMVICYSGILKTLRCRNEKGHR 240
Db      181 CQEDSVTCGPYPFRGMNNFHTMRLVPLLIMVICYSGILKTLRCRNEKGHR 240
Qy      241 AYRVTIMIVYLFWTPNIVILLNTFOEFFLSNCESTSOLDQATOVTETLGMTHCCI 300
Db      241 AYRVTIMIVYLFWTPNIVILLNTFOEFFLSNCESTSOLDQATOVTETLGMTHCCI 300
Qy      301 NPIIYAFGEKEFRLSYVPRKRITKRPCKOCVPYRBTVDGTSTNTPSTGEQEVSAGL 360
Db      301 NPIIYAFGEKEFRLSYVPRKRITKRPCKOCVPYRBTVDGTSTNTPSTGEQEVSAGL 360

```

Query Match	100.0%	Score 1900;	DB 8;	Length 360;
Best Local Similarity	100.0%	Pred. No. 1..9e-206;		
Matches	360;	Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0;

```

Qy      1 MLSTSRSPRINTNESEBEVTTFFDYDGAPEKRFDVQIGAQOLPPPLSIVFPGVGN 60
Db      1 MLSTSRSPRINTNESEBEVTTFFDYDGAPEKRFDVQIGAQOLPPPLSIVFPGVGN 60
Qy      61 MLVVLINCKLKCLTDIYLLNIAISDLFLITLPLWAHSAANEWVGNAMCKLFGLY 120
Db      61 MLVVLINCKLKCLTDIYLLNIAISDLFLITLPLWAHSAANEWVGNAMCKLFGLY 120
Qy      121 HIGYFGGIPPIIILIDRYLAIVHAFALKARTTGFVTSVITMLVAVASVPGIIFTK 180
Db      121 HIGYFGGIPPIIILIDRYLAIVHAFALKARTTGFVTSVITMLVAVASVPGIIFTK 180
Qy      181 CQEDSVTCGPYPFRGMNNFHTMRLVPLLIMVICYSGILKTLRCRNEKGHR 240
Db      181 CQEDSVTCGPYPFRGMNNFHTMRLVPLLIMVICYSGILKTLRCRNEKGHR 240
Qy      241 AYRVTIMIVYLFWTPNIVILLNTFOEFFLSNCESTSOLDQATOVTETLGMTHCCI 300
Db      241 AYRVTIMIVYLFWTPNIVILLNTFOEFFLSNCESTSOLDQATOVTETLGMTHCCI 300
Qy      301 NPIIYAFGEKEFRLSYVPRKRITKRPCKOCVPYRBTVDGTSTNTPSTGEQEVSAGL 360
Db      301 NPIIYAFGEKEFRLSYVPRKRITKRPCKOCVPYRBTVDGTSTNTPSTGEQEVSAGL 360

```

XX RESULT 8
 ADL82831 ID ADL82831 standard; protein: 360 AA.
 XX AC ADL82831;
 XX DT 17-JUN-2004 (first entry)
 XX DB Human PRO84690, SEQ ID 33.

XX KW Immunosuppressive; Cytoplastic; Antiarthritic; Antirheumatic; Antianemic;
 XX RW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
 XX Gene Therapy; PRO; B cell related disorder; cancer;

KW immune-mediated inflammatory disease; human.
XX OS Homo sapiens.
XX WO2004024097-A2.
XX PN 25-MAR-2004.
XX PD 15-SEP-2003; 2003WO-US029097.
XX PF 16-SEP-2002; 2002US-0411392P.
XX PR (GETH) GENENTECH INC.
XX PA Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI,
PI Wu TD;
XX WPI: 2004-329389/30.
DR N-PSDB; ADL82830.
XX PT New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anaemia, myasthenia gravis or ankylosing spondylitis.
XX PT XX
PS Claim 10; Fig 33; 695pp; English.
XX The present invention relates to PRO proteins and their coding sequences. The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide antigen unresponsiveness, selective IgA deficiency, selective IgM deficiency, selective deficiency of IgG subclasses, immunodeficiency with hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's lymphoma, intermediate lymphoma, follicular lymphoma, type II hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic anaemia, myasthenia gravis, glomerulonephritis, or ankylosing spondylitis. The PRO proteins are also useful for preparing a medicament for treating a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
XX Sequence 360 AA:
SQ 121 HIGYFGGIGIFFIILITIDYLAIHVAFALKARTVTFGVTVTITWLVAVFASVPGIFTK 180
Query Match Score 1900; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 1..9e-206;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MUSTSRSRPIRNTNESGEVTTPDYGA~~PCKFDVKQIQGLQPLPYSVLFIGTVGN~~ 60
1 MUSTSRSRPIRNTNESGEVTTPDYGA~~PCKFDVKQIQGLQPLPYSVLFIGTVGN~~ 60
Qy 61 MLVVLILINCKKLKCLTDIYLLNIAISDILFLITLPIWAHSAANEWFGNAMCKLFGTLY 120
61 MLVVLILINCKKLKCLTDIYLLNIAISDILFLITLPIWAHSAANEWFGNAMCKLFGTLY 120
Db 121 HIGYFGGIGIFFIILITIDYLAIHVAFALKARTVTFGVTVTITWLVAVFASVPGIFTK 180
Db 121 HIGYFGGIGIFFIILITIDYLAIHVAFALKARTVTFGVTVTITWLVAVFASVPGIFTK 180
Qy 181 CQEDSVYVCGPYPPRGNNNFTIMRNLLGVLPLLIMVICYSGILTKLRCNEKGRHR 240
181 CQEDSVYVCGPYPPRGNNNFTIMRNLLGVLPLLIMVICYSGILTKLRCNEKGRHR 240
Db 181 AVRVFTIMIVYFLWTPNIVILLNTQEFGNSNCESTSOLDQATQVTEFLGMTHCC1 300
Qy 241 AVRVFTIMIVYFLWTPNIVILLNTQEFGNSNCESTSOLDQATQVTEFLGMTHCC1 300
Db 241 AVRVFTIMIVYFLWTPNIVILLNTQEFGNSNCESTSOLDQATQVTEFLGMTHCC1 300
Db 301 NPIIYAFVGEKFRLSVPFRKHTKQCTVYFRETVDGYTSNTTPSTGQEVSAGL 360
Qy 301 NPIIYAFVGEKFRLSVPFRKHTKQCTVYFRETVDGYTSNTTPSTGQEVSAGL 360
Db 301 NPIIYAFVGEKFRLSVPFRKHTKQCTVYFRETVDGYTSNTTPSTGQEVSAGL 360

RESULT 9
AAU07613 standard; protein; 360 AA.
XX ID AAU07613;
AC AAU07613;
XX DT 04-DEC-2001 (first entry)
XX Human CCR2-64I polymorphic variant polypeptide.
XX Human; CCR2 receptor; CCR2-64I; CCR2-64V; gene therapy; atherosclerosis; single nucleotide polymorphism; hypercholesterolaemia.
XX Homo sapiens.
XX Key FH Location/Qualifiers
Misc-difference 64
FT /note= "Wild-type Val is replaced by Ile."
XX PN WO200162796-A1.
XX PD 30-AUG-2001.
XX PR 22-FEB-2001; 2001WO-GB0000755.
XX PR 22-FEB-2000; 2000GB-00004183.
XX PA (SMIK) SMITHKLINE BRECHAM PLC.
XX PI Valdes AM, Groot PHE, Spurr NK;
XX DR WPI: 2001-550086/61.
DR N-PSDB; AAS12139.
XX Diagnosing atherosclerosis or susceptibility to atherosclerosis in a subject, by determining a single nucleotide polymorphism in specific codon of a polynucleotide encoding human CCR2 receptor in genome of the subject.
XX PS Claim 1; Page 20; 28pp; English.
XX The invention relates to diagnosing atherosclerosis (or susceptibility to) in a subject by determining expression or activity of the human CCR2-64I polypeptide (a polymorphic variant form of the human CCR2 receptor or the CCR2-64V polypeptide (human CCR2 receptor), by screening for a single nucleotide polymorphism in codon 64 of the polynucleotide encoding the CCR2 receptor. This results in production of CCR2-64I, whereby polymorphic variants are associated with a lower incidence of atherosclerosis. The presence or amount of CCR2-64I/V in a sample can also be analysed. The sequences of the invention can be used for predicting the response of a patient to drug treatment, for predicting the disease outcome in a patient and also for the production of a treatment for hypercholesterolaemia. The sequence represents the polymorphic variant polypeptide CCR2-64I sequence 360 AA:
SQ Query Match Score 1899; DB 4; Length 360;
Best Local Similarity 99.9%; Pred. No. 2.4e-206;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MUSTSRSRPIRNTNESGEVTTPDYGA~~PCKFDVKQIQGLQPLPYSVLFIGTVGN~~ 60
1 MUSTSRSRPIRNTNESGEVTTPDYGA~~PCKFDVKQIQGLQPLPYSVLFIGTVGN~~ 60
Db 61 MLVVLILINCKKLKCLTDIYLLNIAISDILFLITLPIWAHSAANEWFGNAMCKLFGTLY 120
61 MLVVLILINCKKLKCLTDIYLLNIAISDILFLITLPIWAHSAANEWFGNAMCKLFGTLY 120
Qy 121 HIGYFGGIGIFFIILITIDYLAIHVAFALKARTVTFGVTVTITWLVAVFASVPGIFTK 180
Db 121 HIGYFGGIGIFFIILITIDYLAIHVAFALKARTVTFGVTVTITWLVAVFASVPGIFTK 180
Qy 181 CQEDSVYVCGPYPPRGNNNFTIMRNLLGVLPLLIMVICYSGILTKLRCNEKGRHR 240
181 CQEDSVYVCGPYPPRGNNNFTIMRNLLGVLPLLIMVICYSGILTKLRCNEKGRHR 240
Db 181 AVRVFTIMIVYFLWTPNIVILLNTQEFGNSNCESTSOLDQATQVTEFLGMTHCC1 300
Qy 241 AVRVFTIMIVYFLWTPNIVILLNTQEFGNSNCESTSOLDQATQVTEFLGMTHCC1 300
Db 241 AVRVFTIMIVYFLWTPNIVILLNTQEFGNSNCESTSOLDQATQVTEFLGMTHCC1 300
Db 61 MLVVLILINCKKLKCLTDIYLLNIAISDILFLITLPIWAHSAANEWFGNAMCKLFGTLY 120
Qy 61 MLVVLILINCKKLKCLTDIYLLNIAISDILFLITLPIWAHSAANEWFGNAMCKLFGTLY 120
Db 61 MLVVLILINCKKLKCLTDIYLLNIAISDILFLITLPIWAHSAANEWFGNAMCKLFGTLY 120
Qy 121 HIGYFGGIGIFFIILITIDYLAIHVAFALKARTVTFGVTVTITWLVAVFASVPGIFTK 180
Db 121 HIGYFGGIGIFFIILITIDYLAIHVAFALKARTVTFGVTVTITWLVAVFASVPGIFTK 180

Qy	181	CQEDSVVYCGPYPPRGWNPNFTTMRNLLGVLPLIMIVCYSGILKTLJRCRNEKGHR	240		Qy	121	HIGYFGGIPIIILITIDRYLAIYHAVAFLKARTYTFGVTSVITWLVAYPASVPGIIFTK	180
Db	181	CQEDSVVYCGPYPPRGWNPNFTTMRNLLGVLPLIMIVCYSGILKTLJRCRNEKGHR	240		Db	121	HIGYFGGIPIIILITIDRYLAIYHAVAFLKARTYTFGVTSVITWLVAYPASVPGIIFTK	180
Qy	241	AVRVIPTIMIVYPLFNTPTPNVILLANTPQQEFGLNCESTSQLQATOVTETLGMTHCCJ	300		Qy	181	CQEDSVVYCGPYPPRGWNPNFTTMRNLLGVLPLIMIVCYSGILKTLJRCRNEKGHR	240
Db	241	AVRVIPTIMIVYPLFNTPTPNVILLANTPQQEFGLNCESTSQLQATOVTETLGMTHCCJ	300		Db	181	CQEDSVVYCGPYPPRGWNPNFTTMRNLLGVLPLIMIVCYSGILKTLJRCRNEKGHR	240
Qy	301	NPIIYAFVGKEFPRYLISVFKHITKRFCKOCPVYRETYDGVTSINTPGEQEVSAGL	360		Qy	241	AVRVIPTIMIVYPLFNTPTPNVILLANTPQQEFGLNCESTSQLQATOVTETLGMTHCCJ	300
Db	301	NPIIYAFVGKEFPRYLISVFKHITKRFCKOCPVYRETYDGVTSINTPGEQEVSAGL	360		Db	241	AVRVIPTIMIVYPLFNTPTPNVILLANTPQQEFGLNCESTSQLQATOVTETLGMTHCCJ	300
RESULT 10								
	ABB56340	standard; protein; 360 AA.						
XX	ABB56340;							
AC								
XX								
DT	18-FEB-2002	(first entry)						
DE								
XX								
XX								
XX								
KW	Non-endogenous human GPCR protein, SEQ ID NO: 473.							
KW	Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;							
KW	constitutively activated GPCR; agonist; disease.							
XX								
OS	Homo sapiens.							
OS	OS							
Synthetic.								
XX								
PN	WO2001177172-A2.							
XX								
PD	18-OCT-2001.							
XX								
PP	05-APR-2001; 2001WO-US011098.							
XX								
PR	07-APR-2000; 2000US-0195747P.							
XX								
XX								
PA	(AREN-) ARENA PHARM INC.							
XX								
PI	Lehmann-Bruinsma K, Liaw CW, Lin I;							
XX								
DR	WPI; 2001-648759/74.							
XX								
DR	N-PSDB; ABI97976.							
XX								
PT	Identifying agonists of G protein-coupled receptors (GPCRs) for use in							
PT	disease treatment, comprises contacting candidate compounds with versions							
PT	of GPCRs.							
XX								
PS	Claim 1; Page 274-275; 394pp; English.							
XX								
CC	The invention relates to G protein-coupled receptors (GPCRs) for which							
CC	the endogenous ligand has been identified. Non-endogenous constitutively							
CC	activated versions of known GPCRs are used in the invention for the							
CC	direct identification of candidate compounds as receptor agonists,							
CC	inverse agonists or partial agonists. Such agonists are useful as							
CC	therapeutic agents for diseases or disorders associated with GPCRs. The							
CC	present sequence is a non-endogenous version of a known human GPCR							
XX	Sequence 360 AA;							
SQ	Query Match 99.7%; Score 1894; DB 4; Length 360;							
	Best Local Similarity 99.7%; Pred. No. 8.9e-206;							
	Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;							
Qy	1	MLSTSRSPTRNTNESGEETTFFPDYDAPCHKDVKQLAQQLPPLYSVTFGFVGN	60					
Db	1	MLSTSRSPTRNTNESGEETTFFPDYDAPCHKDVKQLAQQLPPLYSVTFGFVGN	60					
SQ	Query Match 96.7%; Score 1638; DB 7; Length 347;							
	Best Local Similarity 100.0%; Pred. No. 1.9e-199;							
	Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Qy	61	MLVVLILINCKKLKCLTDIYLNLAISDIIFLITLPLWAHSAAANEWVNAMCQLFTGLY	120					
Db	61	MLVVLILINCKKLKCLTDIYLNLAISDIIFLITLPLWAHSAAANEWVNAMCQLFTGLY	120					

QY 14 NESGEEVITFPDYDYGAPCHKDVKOIGAQQLLPPLYSLVIFGFVGNNMLVVLILINCKKL 73
 DR DR; WPI; 1995-263866/34.
 Db XX
 1 NESCDEVITFPDYDYGAPCHKDVKIQAQLLPPLYSLVIFPFGVNLVVLILINCKKL 60
 PT PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
 QY 74 KCLTDIYLNLALISDLFLFLITPLWAHSAAANEVFGNAMCKLFTGGLYTHGYFGGIFFIL 133
 PR PR for identifying antagonists and for treating diseases characterised by
 monocytic infiltrates.
 Db XX
 AC Claim 2; Fig 1; 84pp; English.

QY 134 LTIDRYLAIVHAIFALKARTTGTGVTSTVTLVAVFASPGIIFTKQKEQSIVTVCGPY 193
 CC To identify and clone new members of the chemokine receptor gene family,
 CC degenerate oligo primers were designed corresp. to the conserved
 CC sequences R79167 in the second and R79168 in the third transmembrane
 CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the
 CC HUMSTRS orphan receptor (GenBank Accession #M94293). The degenerate oligo
 CC incorporating EcoRI and XbaI sites at their 5' ends are Q96299 and
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers
 CC yielded a number of PCR products. One cDNA appeared to encode a novel
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA
 CC library was constructed in pPROG and probed with the PCR product. A 2.1
 CC kb cDNA clone was obt. Analysis of additional clones in the MM6 cDNA
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA
 CC sequence first obt. from the 5' UTR through the putative seventh
 CC transmembrane domain but contained a different cytoplasmic tail. The
 CC second sequence appears to represent alternative splicing of the carboxyl
 CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-
 CC 1RA and MCP-1RB (see Q96299/R79165 & Q96298/R79166). Active mature MCP-
 CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.
 CC wt. of about 41,000 daltons. (updated on 25-MAR-2003 to correct PN
 CC field.)
 XX

Db Sequence 374 AA;

QY Query Match 86.9%; Score 1651.5; DB 2; Length 374;
 Best Local Similarity 95.5%; Pred. No. 3 1e-178;
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Db 1 MUSTRSRSRIRNTNESEGVETTFFDYDYGAPCHKDVKIQAQLLPPLYSLVIFGTVGN 60
 1 MUSTRSRSRIRNTNESEGVETTFDYGAPCHKDVKIQAQLLPPLYSLVIFGTVGN 60

QY 254 LFNTPYNIVLILNTFOBPFGLSNCESTSOLDATQVTBTGLMTHCCINPIITYAFVGKEKFR 313
 Db 241 LFNTPYNIVLILNTFOBPFGLSNCESTSOLDATQVTBTGLMTHCCINPIITYAFVGKEKFR 300

QY 314 RYLSVFEFRKHITKRFKCQCPVFRETDGVTSTNTPSGEQTSAGL 360
 Db 301 RYLSVFEFRKHITKRFKCQCPVFRETDGVTSTNTPSGEQTSAGL 347

RESULT 12
 ID AAR79165 standard; protein; 374 AA.
 XX
 AC AAR79165;
 XX DT 25-MAR-2003 (revised)
 DT 29-DEC-1995 (first entry)
 XX DE Human monocyte chemoattractant protein-1 receptor MCP-1RA.
 XX KW Monocyte chemoattractant protein-1 receptor; MCP-1R; chemokine.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 1..48
 FT Domain /label= extracellular
 FT Domain 49..70
 FT Domain /label= transmembrane
 FT Domain 80..700
 FT Domain /label= transmembrane
 FT Domain 115..136
 FT Domain /label= transmembrane
 FT Domain 154..178
 FT Domain /label= transmembrane
 FT Domain 204..231
 FT Domain /label= transmembrane
 FT Domain 244..268
 FT Domain /label= transmembrane
 FT Domain 295..313
 FT Region /label= transmembrane
 FT Region 314..375
 FT Region /label= carboxyl tail
 XX PN W09519436-A1.
 XX PD 20-JUL-1995.
 XX PF 11-JAN-1995; 95NO-US000476.
 XX PR 13-JAN-1994; 94US-00182962.
 XX PA (REGC) UNIV CALIFORNIA.
 PA Charo I, Coughlin S;
 PI XX
 KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;

Db RESULT 13
 ID AAC80107
 XX AAC80107 standard; protein; 374 AA.
 AC AAC80107;
 XX DT 17-JAN-2002 (first entry)
 DE Human CCR2a protein.
 KW

KW	chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW	antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW	antirheumatic; antiarthritic.
XX	
OS	Homo sapiens.
XX	
PN	WO200172330-A2.
XX	
PD	04-OCT-2001.
XX	
PP	02-APR-2001; 2001W0-EP003708.
XX	
PR	31-MAR-2000; 2000DE-01016013.
XX	
(IPPP-)	IPF PHARM GMBH.
PA	(FORS/) FORSSMANN U.
XX	
PI	Forssmann W, Adermann K, Heitland A, Spodsborg N;
XX	
DR	WPI; 2001-626256/72.
XX	
PT	Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.
PT	
PS	Disclosure; Page 9; 26pp; German.
XX	
CC	This invention describes a novel diagnostic agent (I) comprising at least two different ligands (II) for receptors (III) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus), where the (cardio)vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antiviral, antirheumatic, immunosuppressive, dermatological, antiasthmatic, antiarthritic.
CC	Chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (CR), which control migration and proliferation of these cells. AA80045-AAG80128 represent human chemokine fragments used to illustrate the method of the invention
XX	
SQ	Sequence 374 AA;
Query Match	86.9%; Score 1651.5; DB 4; Length 374;
Best Local Similarity	95.5%; Pred. No. 3.1e-178;
Matches	319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;
Db	1 MLSTSRSRFRNTNESGEVTTFPDYGAPCKPDKDQIGAQOLPPPLSVPIFGFTGN 60
Db	1 MLSTSRSRFRNTNESGEVTTFPDYGAPCKPDKDQIGAQOLPPPLSVPIFGFTGN 60
Qy	61 MLVVLILINKKKLCLTDYLLNIAISDLFLITLPLWAHSAAANEWFGNAMCKLFTGLY 120
Db	61 MLVVLILINKKKLCLTDYLLNIAISDLFLITLPLWAHSAAANEWFGNAMCKLFTGLY 120
Qy	121 HIGYGGIPIFFLITIDRYLAIVHAFALKARTYEGVYTTSVTLVAVFASVPGIIFTK 180
Db	121 HIGYGGIPIFFLITIDRYLAIVHAFALKARTYEGVYTTSVTLVAVFASVPGIIFTK 180
Qy	181 CQEDSVTYCGPYPPRGNNFHITMRNLIGLVLLIMIVCYSILKLTLCRNNEKGHR 240
Db	181 CQEDSVTYCGPYPPRGNNFHITMRNLIGLVLLIMIVCYSILKLTLCRNNEKGHR 240
Qy	241 AVRIFTIMIVYFLWTPNIVILNTFOFGUSNCSTSQLQATOVTETLGTMTHCCI 300
Db	241 AVRIFTIMIVYFLWTPNIVILNTFOFGUSNCSTSQLQATOVTETLGTMTHCCI 300
Qy	301 NPIIYAFVGKERRYLSVFRKHITKRFCKQCVP 334
Db	301 NPIIYAFVGKERRYLSVFRKHITKRFCKQCVP 334
Qy	301 NPIIYAFVGKEREK--SLP--HTALG-CRIPL 327
Db	61 MLVVLILINKKKLCLTDYLLNIAISDLFLITLPLWAHSAAANEWFGNAMCKLFTGLY 120
Qy	121 HIGYGGIPIFFLITIDRYLAIVHAFALKARTYEGVYTTSVTLVAVFASVPGIIFTK 180
Query Match	86.9%; Score 1651.5; DB 6; Length 374;
Best Local Similarity	95.5%; Pred. No. 3.1e-178;
Matches	319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;
Db	1 MLSTSRSRFRNTNESGEVTTFPDYGAPCKHFKDQIGAQOLPPPLSVPIFGFTGN 60
Db	1 MLSTSRSRFRNTNESGEVTTFPDYGAPCKHFKDQIGAQOLPPPLSVPIFGFTGN 60
Qy	61 MLVVLILINKKKLCLTDYLLNIAISDLFLITLPLWAHSAAANEWFGNAMCKLFTGLY 120
Db	61 MLVVLILINKKKLCLTDYLLNIAISDLFLITLPLWAHSAAANEWFGNAMCKLFTGLY 120

Db 121 HIGFGGIFFIILTIDRYLAIHAVFALKARTVTGVTVSITWLVAVFASVPGIIFTK 180
 Qy 181 CQEDSVYVGPFPRGMNNFPTIMRNLLGVLPLIMIVCYSGILKTLRRCNEKEKRR 240
 Db 181 CQEDSVYVGPFPRGMNNFPTIMRNLLGVLPLIMIVCYSGILKTLRRCNEKEKRR 240
 Qy 241 AYRIFTIMIVYLFWTPNIVILLNTQFFGLSNCESTSSQLDQATQVTELGTMHCCI 300
 Db 241 AYRIFTIMIVYLFWTPNIVILLNTQFFGLSNCESTSSQLDQATQVTELGTMHCCI 300
 Qy 301 NPIYAFGEKFRRLSYFPRKHITKRFCKQCPV 334
 Db 301 NPIYAFGEKFR---SLF---HIALG-CR RIAPL 327

RESULT 15
 ADD44861 ID ADD44861 standard; protein; 374 AA.
 XX AC ADD44861;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human Protein P41597, SEQ ID NO 10292.
 XX KW Human; pain; neuronal tissue; gene therapy;
 spinal segmental nerve injury; chronic constriction injury; CCI;
 spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX PI Woolf C, D'urso D, Befort K, Costigan M;
 XX DR WPI: 2003-268312/26.
 DR GENBANK; P41597.

XX PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
 PT preparing a medicament for treating pain in an animal.
 PS Claim 1; Page: 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more

polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at Etp.wipo.int/pub/published_pct_sequences.

SQ Sequence 374 AA;

	Query Match	Score 1651.5;	DB 7;	Length 374;
	Best Local Similarity	95.5%;	Pred. No. 3..le-18;	
Matches	Conservative	3;	Mismatches	5;
	Indels	7;	Gaps	3;
Qy	1	MULSTRSRSPRINTNESSEBEVTTFDDYDGAPCHKFVDKIQGAQLPLPOLYSLVIFGGVGN 60		
Db	1	MULSTRSRSPRINTNESSEBEVTTFPDMDYDGAPCHKFVDKIQGAQLPLPOLYSLVIFGGVGN 60		
Qy	61	MIVVLLILINCKKLKCLTDIYLNLALASDLFLFLJLTPWAHSAAANEVFGNAMCKLFLTGLY 120		
Db	61	MIVVLLILINCKKLKCLTDIYLNLALASDLFLFLJLTPWAHSAAANEVFGNAMCKLFLTGLY 120		
Qy	121	HIGYFGGIFFPILLITDRLAYIAHVAFALKARTVTFGVTSVTTWLVAVFASVPGIIFTK 180		
Db	121	HIGYFGGIFFPILLITDRLAYIAHVAFALKARTVTFGVTSVTTWLVAVFASVPGIIFTK 180		
Qy	181	CQKEDSYTYVCGPVFPRGMNNFPTIMRNLLGVLPLIMIVCYSGILKTLRRCNEKEKRR 240		
Db	181	CQKEDSYTYVCGPVFPRGMNNFPTIMRNLLGVLPLIMIVCYSGILKTLRRCNEKEKRR 240		
Qy	241	AYRIFTIMIVYLFNTPYNIVILLNTQFFGLSNCESTSSQLDQATQVTELGTMHCCI 300		
Db	241	AYRIFTIMIVYLFNTPYNIVILLNTQFFGLSNCESTSSQLDQATQVTELGTMHCCI 300		
Qy	301	NPIIYAFGEKFRRLSYFPRKHITKRFCKQCPV 334		
Db	301	NPIIYAFGEKFRRLSYFPRKHITKRFCKQCPV 334		

Search completed: June 9, 2005, 16:44:16
 Job time : 112.826 Secs

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Run on: June 9, 2005, 16:29:43 ; Search time 25.0136 Seconds
 (without alignments)
 1384.767 Million cell updates/sec

Title: US-10-791-166-4
 Perfect score: 1900
 Sequence: 1 MLSTSRSPRINTNSEEV.....DGVTSTNTPTQEVSAGL 360

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database: PIR 79:*

- 1: pix1:*
- 2: pix2:*
- 3: pix3:*
- 4: pix4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1900	100.0	360	JC2443	chemokine (C-C) receptor
2	1651.5	86.9	374	I38450	chemokine (C-C) receptor
3	1364	71.8	352	A43113	chemokine (C-C) receptor
4	1036	54.5	355	R45177	MIP-1 alpha receptor
5	1010.5	53.2	359	I49341	macrophage inflammatory protein-1
6	963.5	50.7	355	I49339	chemokine (C-C) receptor
7	951	50.1	355	G02436	chemokine (C-C) receptor
8	871	45.8	360	JC4587	chemokine (C-C) receptor
9	862.5	45.4	360	I5160	chemokine (C-C) receptor
10	822.5	43.3	383	S55594	G protein-coupled receptor
11	778.5	41.0	356	I49340	MIP-1 alpha receptor
12	751	39.5	355	JC5067	G protein-coupled receptor
13	722.5	38.0	354	I58186	probable G protein-coupled receptor
14	708	37.3	355	JC4304	orphan G protein-coupled receptor
15	649.5	34.2	344	I49342	chemokine receptor
16	581.5	30.3	378	B55735	lymphocyte specific receptor
17	569	29.9	378	A55735	G protein-coupled receptor
18	567.5	29.9	378	A45680	G protein-coupled receptor
19	563	29.6	369	JC5068	G protein-coupled receptor
20	547	28.8	360	A53611	interleukin-8 receptor
21	540.5	28.4	355	JQ1231	interleukin-8 receptor
22	540.5	28.4	359	I4921	interleukin-8 receptor
23	536.5	28.2	358	A53752	interleukin-8 receptor
24	532.5	28.0	356	S42096	interleukin-8 receptor
25	532	28.0	367	JB0349	interferon-inducible protein
26	528.5	27.8	333	I65989	G protein-coupled receptor
27	528.5	27.8	350	A39445	interleukin-8 receptor
28	515.5	27.1	352	G0048	neuropeptide Y receptor
29	515	27.1	353	S28787	neuropeptide Y receptor

ALIGNMENTS						
RESULT 1						
JC2443	Chemokine (C-C) receptor 2, splice form B - human	N;Alternative names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1 receptor	PIDN:BAU06251.1;			
C;Species: Homo sapiens (man)	C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004					
C;Accession: JC2443 ; I38463	A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor					
R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.	A;Reference number: JC2443 ; MUID:94324942; PMID:8048929					
Biochem. Biophys. Res. Commun. 202, 1155-1162, 1994	A;Accession: JC2443 ; MUID:9195821; PMID:8146186					
A;Molecule type: mRNA	A;Residues: 1-360 <YAM>					
A;Cross-references: UNIPROT:PA1597; DBPI:D29984; NID:951246; PIDN:BAU06251.1;	A;Cross-references: EMBL:U03905; NID:919120.1; PID:9472558					
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.						
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994						
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors						
A;Reference number: M33477; MUID:94195821; PMID:8146186						
A;Accession: I38463						
A;Status: preliminary						
A;Molecule type: mRNA						
A;Residues: 1-360 <REB>						
A;Cross-references: EMBL:U03905; NID:919120.1; PID:9472558						
C;Genetics:						
A;Gene: GDB:CMCBR2						
A;Cross-references: GDB:337361; OMIM:601267						
A;Map position: 3p21-3p21						
C;Superfamily: vertebrate rhodopsin						
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane #status predicted <TM1>						
F;43-70/Domain: transmembrane #status predicted <TM1>						
F;81-100/Domain: transmembrane #status predicted <TM2>						
F;115-136/Domain: transmembrane #status predicted <TM3>						
F;154-178/Domain: transmembrane #status predicted <TM4>						
F;207-226/Domain: transmembrane #status predicted <TM5>						
F;244-268/Domain: transmembrane #status predicted <TM6>						
F;287-309/Domain: transmembrane #status predicted <TM7>						
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted						
F;113-190/Disulfide bonds: #status predicted						
Query Match Score 100.0%; Score 1900; DB 2; Length 360;						
Best Local Similarity 100.0%; Pred. No. 1..6-156; Mismatches 0; Indels 0; Gaps 0;						
Matches 360; Conservative 0;						
Qy 1 MLSTSRSPFRNTNSGEETTFPYDYGCPKREDVKQGAQLLPLVSFLVFGFVG 60						
Db 1 MLSTRSRSPFRNTNSGEETTFPYDYGCPKREDVKQGAQLLPLVSFLVFGFVG 60						
Qy 61 MLVVILINCKKLCKLDTIYLNLASIDLFLITPLWAHSAAANWFGNAMCKLFTGTLY 120						
Db 61 MLVVILINCKKLCKLDTIYLNLASIDLFLITPLWAHSAAANWFGNAMCKLFTGTLY 120						

Qy	121	HIGYFGGIFFFIILTIDRYLAIVHVAFLKARTVTFGIVVSVITWLVAFASVPGILFTK	180	Qy	301	NPIIYAFVGEKFRYLSSVFRKHITKRFCKOCPV	334
Db	121	HIGYFGGIFFFIILTIDRYLAIVHVAFLKARTVTFGIVVSVITWLVAFASVPGILFTK	180	Db	301	NPIIYAFVGEKFR - SLP -- HIALG-CRIAPL	327
Qy	181	CQEDSVTVCGPFPRGNNNFTIMNLLGVLPLIMIVCYSGILTKLRLCRNEKCRHR	240				
Db	181	CQEDSVTVCGPFPRGNNNFTIMNLLGVLPLIMIVCYSGILTKLRLCRNEKCRHR	240				
	RESULT 3						
	A43113	chemokine (C-C) receptor 5 - human N;Alternative names: C-C CRHR-5; CCRS5 C;Species: Homo sapiens (man)					
Qy	241	AVRIFTMIVVYFLFWTPNIVLNTFOFFGLSNCSTSQLDQATOVTETLGTMTHCC1	300	C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000 C;Accession: A43113; S71808; A56834; A58832; G02653; A56833 R;Samson, M.; Labbe, O.; Mollierau, C.; Vassart, G.; Parmentier, M.			
Db	241	AVRIFTMIVVYFLFWTPNIVLNTFOFFGLSNCSTSQLDQATOVTETLGTMTHCC1	300	R;Biochemistry 35: 3362-3367, 1996 A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor A;Reference number: S71808; MUID:96345670; PMID:8639485			
Qy	301	NPIIYAFVGEKFRYLSSVFRKHITKRFCKQCPFYRETVDGV7ISTNPSTGEVSAGL	360	A;Accession: A43113; MUID: A43113; PMID: 8639485			
Db	301	NPIIYAFVGEKFRYLSSVFRKHITKRFCKQCPFYRETVDGV7ISTNPSTGEVSAGL	360	A;Accession type: mRNA A;Residues: 1-352 <SAM1>			
	RESULT 2			A;Cross-references: GB:X91492; NID:91262810; PID:CAA62796.1; PID:91262811 R;Samson, M.; Libert, F.; Doran, B.J.; Rucker, J.; Lieberard, C.; Farber, C.M.; Saragosti, M.; Inai, T.; Rana, S.; Yl, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa			
I38450		Chemokine (C-C) receptor 2, splice form A - human Chemokine receptor; monocyte chemoattractant protein 1 receptor; monocyte chemokine receptor 2; monocyte chemoattractant protein 1 receptor; monocyte chemokine receptor N;Alternative names: C-C CRHR-2; CCSP2 C;Species: Homo sapiens (man)		C;Date: 16-Feb-1996 #sequence revision 16-Feb-1996 #text_change 09-Jul-2004 C;Accession: I38450 R;Charno, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R. Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994 A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane A;Reference number: A53477; MUID:94195821; PMID:8146186			
				A;Accession: I38450 A;Molecule type: mRNA A;Residues: 1-374 <RES> A;Cross-references: UNIPROT:P41597; EMBL:U03882; NID:9472555; PID:AAA19119.1; PID:947255 C;Genetics: A;Gene: GDB:CMKBR2 A;Cross-references: GDB:337364; OMIM:601267 A;Map position: 3p21-3p21 C;Superfamily: vertebrate rhodopsin C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane F:44-68/Domain: transmembrane #status predicted <TM1> F:79-99/Domain: transmembrane #status predicted <TM3> F:114-178/Domain: transmembrane #status predicted <TM4> F:208-226/Domain: transmembrane #status predicted <TM5> F:244-268/Domain: transmembrane #status predicted <TM6> F:292-309/Domain: transmembrane #status predicted <TM7> F:14/Binding site: carbohydrate (Nan) (covalent) #status predicted F:34-277,113-190/Disulfide bonds:			
				Query Match Score 86.9%; DB 2; Length 374; Best Local Similarity 95.5%; Pred. No. 4.8e-135; Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;			
Qy	1	MLSTSRSRFLRNTNESGEETTPFDYDGPCKHDVKQGAQQLPPLYSLVPLFGFVN	60	Qy	1	HIGYFGGIFFILLTIDRYLAIVHVAFLKARTVTFGIVVSVITWLVAFASVPGILFTK	180
Db	1	MLSTSRSRFLRNTNESGEETTPFDYDGPCKHDVKQGAQQLPPLYSLVPLFGFVN	60	Db	1	HIGYFGGIFFILLTIDRYLAIVHVAFLKARTVTFGIVVSVITWLVAFASVPGILFTK	180
Qy	61	MLVVTLINKCKLKCLTDIVLNLAISDLFLITPLWAAANEWVGNAMCKLFTGLY	120	Qy	121	HIGYFGGIFFILLTIDRYLAIVHVAFLKARTVTFGIVVSVITWLVAFASVPGILFTK	180
Db	61	MLVVTLINKCKLKCLTDIVLNLAISDLFLITPLWAAANEWVGNAMCKLFTGLY	120	Db	121	HIGYFGGIFFILLTIDRYLAIVHVAFLKARTVTFGIVVSVITWLVAFASVPGILFTK	180
Qy	121	QKEDSVTVCGPFPRGNNNFTIMNLLGVLPLIMIVCYSGILTKLRLCRNEKCRHR	240	Qy	181	QKEDSVTVCGPFPRGNNNFTIMNLLGVLPLIMIVCYSGILTKLRLCRNEKCRHR	240
Db	121	QKEDSVTVCGPFPRGNNNFTIMNLLGVLPLIMIVCYSGILTKLRLCRNEKCRHR	240	Db	181	QKEDSVTVCGPFPRGNNNFTIMNLLGVLPLIMIVCYSGILTKLRLCRNEKCRHR	240
Qy	241	AVRIFTMIVVYFLFWTPNIVLNTFOFFGLSNCSTSQLDQATOVTETLGTMTHCC1	300	Qy	241	AVRIFTMIVVYFLFWTPNIVLNTFOFFGLSNCSTSQLDQATOVTETLGTMTHCC1	300
Db	241	AVRIFTMIVVYFLFWTPNIVLNTFOFFGLSNCSTSQLDQATOVTETLGTMTHCC1	300	Db	241	AVRIFTMIVVYFLFWTPNIVLNTFOFFGLSNCSTSQLDQATOVTETLGTMTHCC1	300

F;67-87/Domain: transmembrane #status predicted <TM2>
 P;103-124/Domain: transmembrane #status predicted <TM3>
 P;142-166/Domain: transmembrane #status predicted <TM4>
 P;236-257/Domain: transmembrane #status predicted <TM5>
 P;285-300/Domain: transmembrane #status predicted <TM6>
 P;268/Binding site: disulfide bonds #status predicted
 P;336-337,343/Binding site: carbohydrate (Asn) (covalent) #status predicted
 P;340-343/Binding site: phosphate (Thr) (covalent) #status predicted
 P;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match	Score	Length	DB 2;	DB 2;	Length	355;
Best Local Similarity	71.8%		Score 1364;	Pred. No. 3e-110;	Indels	6;
Matches	259;	Conservative	2;	Mismatches	46;	Gaps

Qy 24 FDYKDPYQIGQKQPLPPSLYVTFGVGNMLVLVLLINCKLKLTDIYL 81
 Db 10 YDINYTTSEPCOKINTQIAARLLPLPSLVTFGVGNMLVLVLLINCKLKSMTDIYL 69

Qy 82 LNLAISDPLPLITPLWAHSAAANEMVFGNAMCKLFTGLYHIGYFGGIFPILLTIDRYLA 141
 Db 70 LNLAISDPLPLITPLWAHSAAANEMVFGNAMCKLFTGLYHIGYFGGIFPILLTIDRYLA 129

Qy 142 IYHAPVALKARTVTFGTVTSVITWLVAVASVPGIIFTKCKEDSYVCGPYFP---RG 197
 Db 130 VYHAPVALKARTVTFGTVTSVITWLVAVASVPGIIFTKCKEDSYVCGPYFP---RG 189

Qy 198 WNNFHTIMRNTGIVLPIPLINIVCIGLITKLRLCNEKGHRAYRVTFIMIVYFLFWT 257
 Db 190 WKNFQTLKIVLGIPLVPLWVIVCIGLITKLRLCNEKGHRAYRLIFTMIVYFLFWA 249

Qy 258 PYNTVILLNTQEFFCSNSCRSTSQDQATQTYTETLGMTHCINPIIAYVGKEFRRYLS 317
 Db 250 PYNTVILLNTQEFFCSNSCRSTSQDQATQTYTETLGMTHCINPIIAYVGKEFRRYLL 309

Qy 318 VPFKPKHITRCPQCPVPTRETDGVTSNSTPSTGEQEVSGL 360
 Db 310 VFFQKHAIRCKKCSCSTPQCAAPERASVYTRSTGEQEVSGL 352

RESULT 4

A45177 Sequence extracted from NCBI backbone (NCBIP:124876)

Chemokine (C-C) receptor 1 - human
N;Alternate names: C-C CR-1; macrophage inflammatory protein-1-alpha receptorC;Species: Homo sapiens (man)
C;Accession: 145177; 155671 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004R;Note, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993

A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-

A;Reference number: A45177; MUID:91161416; PMID:769328

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Cross-references: UNIPROT:P32246; GB:L10918; NID:g292416; PID:AAA36543.1; PMID:g292417

A;Experimental source: HU60 cells

R;Gao, J.

J. Exp. Med. 177, 1421-1427, 1993

A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha

A;Reference number: 155671; MUID:33240122; PMID:g292417

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-355 <RES>

C;Cross-references: GB:L10918; NID:g292416; PID:AAA36543.1; PMID:g292417

A;Gene: GDB:CMKB1; CMKB1

A;Cross-references: GDB:338446; OMIM:601159

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: diulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; t:

F;36-60/Domain: transmembrane #status predicted <TM1>
 P;71-91/Domain: transmembrane #status predicted <TM2>
 P;108-129/Domain: transmembrane #status predicted
 P;147-171/Domain: transmembrane #status predicted <TM3>
 P;205-223/Domain: transmembrane #status predicted <TM4>
 P;240-264/Domain: transmembrane #status predicted <TM5>
 P;288-305/Domain: transmembrane #status predicted <TM6>
 F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;24-273; 106-183/Disulfide bonds: #status predicted
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match	Score	Length	DB 2;	DB 2;	Length	355;
Best Local Similarity	54.5%;		Score 1036;	Pred. No. 6.4e-82;	Indels	8;
Matches	199;	Conservative	56;	Mismatches	90;	Gaps

Qy 12 NTNESSBVEVTTFDYNGAPCHFKFDYKQIGQOLLPLPLSILVFI FGTVGNMLVLVLIJINCK 71
 Db 5 NTTED-YDTTBFDYGDATPQKVNRERGAQOLLPLPLSILVFGVGNILVLVLYQVK 63

Qy 72 KLKCLTDIVLNLASDPLPLITPLWA-HSAANEKUFGVGNAMCKLFTGLYHIGYFGGIFF 130
 Db 64 RLKNPNTSIYLNLASDPLPLITPLWA-HSAANEKUFGVGNAMCKLTSQFYPLTGlyEIFF 123

Qy 131 ILLTIDRYLAIYHAWALKARTVTGUVTSVITWLAVAFASVPGIIFTKCKEDSVYVC 190
 Db 124 ILLTIDRYLAIYHAWALKARTVTGUVTSVITWLAVAFASVPGIIFTKCKEDSVYVC 183

Qy 191 GPYFP---REWNNTFTTENMILGLVPLPLIIVCISGILTKLRLRNEKEGRHATRVIF 246
 Db 184 SLHFPPESSLREWKLPLPAKUNLPLWLMICITGIIKILLRPNEKE-SKAFLIF 242

Qy 247 TIMIVYFLKTPTPYNWILLNTFQBPFGLSNCEBTSQDQATQTYTETLGMTHCINPIYA 306
 Db 243 VIMIIFLFLWTPYNTLILISVQDFLFTHEEQSRILDAVQVTEIAYTHCCVNPIYA 302

Qy 307 FVGEKPRYLSVFPRKHITKRPCKKOPCPVFTRETDGVTSNTPSTGEQEVSG 359
 Db 303 FVGERPRKYLQLEFIRRVAHLVKWPFLSDRLRERSS-SPSTGEHLSAG 354

RESULT 5

I49341 Alpha receptor like-2 - mouse

C;Species: Mus musculus (house mouse)

C;Accession: 04-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 1749-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokir

A;Reference number: I49339; MUID:35340546; PMID:7542241

A;Accession: I49341

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residue: 1-359 <RES>

A;Cross-references: UNIPROT:Q8K3M7; EMBL:U28406; NID:9881551; PID:g881552

C;Superfamily: vertebrate rhodopsin

Query Match

53.2%; Score 1010.5;

DB 2; Length 359;

Best Local Similarity

53.5%; Pred. No. 1e-79;

Indels

25;

Gaps

6;

Matches

193;

Conservative

62;

Mismatches

81;

Gaps

6;

Query

10 IRNTNESGBEVTTFPDYDGAQPKCHKDVKQIGAQQLPLSILVFGVGNMLVYLILIN 69

Db 8 IKTVYSE--TTPIYEVAPPCCRKRKELGSWLLPLVPIGLGMMVYLILIK 65

Qy 70 CKKLKCLTDIVLNLASDPLPLITPLWAHSAA-NEWFGNAMCKLFTGLYHIGYFGGI 128

Db 66 YRKLOMNTNLYLNLASDPLPLITPLWAHSAA-NEWFGNAMCKLFTGLYHIGYFGGI 125

Qy 129 FPIILITDIDYLAITYHAWALKARTVTGUVTSVITWLAVAFASVPGIIFTKCKEDSVY 188

Db 126 FPIILITDIDYLAITYHAWALKARTVTGUVTSVITWLAVAFASVPGIIFTKCKEDSVY 185

A;Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:9116
 A;Experimental source: thymus
 C;Genetics:
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;7,202,350/Binding site: carbohydrate (Ser) (covalent) (by casein kinase II) #status predicted
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;321/Binding site: phosphate (thr) (covalent) (by protein kinase C) #status predicted
 Query Match Score 45.8%; Best Local Similarity 45.8%; Matches 168; Conservative 71; Mismatches 103; Indels 12; Gaps 5;
 Qy 10 INTNTNSGEETVTPPFDID-YGAPCHRFDPDKVQGAQLLPPSLVFGVERMLVYVLLI 68
 Db 6 VDTDTQDVTNSYSSYFESMPKPCPTKEGIKAFGEVPLPPSLVPLGLFGNSVVTVLFL 65
 Qy 69 NCKKLKCLTDITYLLNLAISDLPLITLPLWAHSAANEWVFENAMCKLFTGLYHIGYFGGI 128
 Db 66 KTKRLKSMTDVLLNLAISDLPLISPPGTYAAADQWVFGT 125
 Qy 129 PPIILITDIDYLAIHVAEALKARTTEFGVYTSVITLVAYAASVPGIIFTKQCOKEDSVI 188
 Db 126 FPIIMLSDIVDTYDYLAIHVAFSPLGGLLSTCVTEHNHT 185
 Qy 189 VCGPYF---PROWNNPTMANGLVPLLIMVCTSGTLLCRNEKKRRAVRI 245
 Db 186 YCKTQYSVNNTTWKVLSSLEINVGLLIPGMLFVYSMIRTQHCKNEKK-NRAVRMI 244
 Qy 246 PTIMIYVFLFATPTPVNIVLANTFOEFGLSNCESTSOLDAQTVTTGMTHCCINPITY 305
 Db 245 FGVVVFLFLGIFTPTPVNVFLLTLEVLDQDTLVEYLDIAQATITLGPHCCINPITY 304
 Qy 306 AFVGKEFRRLVLSVFFRKHITR---FCKQCPVPTFRETVDGVSINTPSGEQS 355
 Db 305 FFLGKEFRKVTQFLFR---TCRGFLVICKCDFLQVSYADMSSSSYTQSTDHD 355

RESULT 9
 A57160
 N;Alternate names: C-C CKR-4
 C;Species: Homo sapiens (man)
 C;Accession: A57160
 R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; J. Biol. Chem., 270, 19495-19500, 1995
 A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDNA; Reference number: A57160; MUID:93370289; PMID:7642634
 A;Status: preliminary; not compared with conceptual translation
 A;Residues: 1-360 <POW>
 A;Cross-references: UNIPROT:P51679; GB:X85740; NID:91370103; PIDN:CAA59743.1; PID:997145
 A;Molecule type: mRNA
 A;Note: source clone K5-5
 C;Genetics:

A;Gene: CMKBR4
 A;Cross-references: GDB:677463
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein; transmembrane; transmembrane #status predicted <TM1> F;40-65/Domain: transmembrane #status predicted <TM2> F;112-133/Domain: transmembrane #status predicted <TM3> F;208-226/Domain: transmembrane #status predicted <TM4> F;243-264/Domain: transmembrane #status predicted <TM5> F;29-308/Domain: transmembrane #status predicted <TM6> F;29-276,110-187/Disulfide bonds: #status predicted
 F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 Query Match Score 45.4%; Best Local Similarity 48.7%; Matches 164; Conservative 67; Mismatches 61; Indels 11; Gaps 4;
 Qy 31 PCHKFDVKQIGAQALPLPLSUVIFGFVGNMLVYVLLINCKLKCDIYLNLAINASDLL 90
 Db 28 PCTKEGIKAFGEFLFLPPLSIVFGVGNLGSVVVLFLFKYKLRSNTDVYLNLAISDLL 87
 Qy 91 FLITLPWLAHSANENVFGNAMCKLFTGLYHIGYFGSIFILLTDRLYLAVHAFALK 150
 Db 88 FVRSFLFWGYAAADQWVFGLGLCKRMISWMTLVGPISGFIFTMLMSDRYLAVHAFSLR 147
 Qy 151 ARTVTRCEVTVTSEVTVWAVAVASVPGIIFTKQCOKEDSVVYCSFYPRKG---WNNEFTIMRN 207
 Db 148 ARTLIGVITSLATWAVAVASLPGGLFSTCYTERHYCKTKYSNSTTAKVLSIEIN 207
 Qy 208 ILGLVLPPLINIVCIGSGLKTLRNEKGRRAVAVFTIMIVYLFWTPTNIVLILNT 267
 Db 208 ILGLVLPPLGIMLFCYSMITRILQHCKNEKK-NKAVMIFAVVVLFGFWTPTNIVLILET 266
 Qy 268 FQEPRGLSNCESTSOLDAQTVTTGMTHCCINPITYAFGEKFRYLSVFPKRHKR 327
 Db 267 LVELEVQDCTFERYLDYIAQATELAFVHCCLNPIIYFFGEKPKYVLOLFK--TCR 323
 Qy 328 ---FCQCPVTFYRETVDGTISTNTSTGEBOVSAGL 360
 Db 324 GLFVLCQYCGLLQIYISADTPSSYQTSTMDELDHDDA 360

RESULT 10
 S55594
 C;Protein-coupled receptor E1 - equine herpesvirus 2
 C;Species: equine herpesvirus 2
 C;Accession: S55594
 C;Database: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
 R;Telford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
 J. Mol. Biol. 249, 520-528, 1995
 A;Title: The DNA sequence of equine herpesvirus 2
 A;Reference number: S55594; MUID:9530251; PMID:7783207
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:089609; GB:U20824; NID:g695172; PIDN: AAC13788.1; PID:g695173
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor
 Query Match Score 43.3%; Best Local Similarity 47.9%; Matches 162; Conservative 60; Mismatches 107; Indels 9; Gaps 4;
 Qy 4 TSSRSRIRNTNSGEVTTFEDYD-GAPCHKFDFVKQIGAQALPLPLSIVFIFGVGNM 61
 Db 32 TTIASIVPSTNSSEDYDDDDVVDYEASAPYKSDDTRLAQVVPALLYLFLFGLGNI 91
 Qy 62 LVVLLINCKLKCDIYLNLAINASDLLPLITLPIWAH-SAAENEWVEGNAMCKLFTGL 119
 Db 92 LVVVIVRYMKIKNTNMNLAINASDLLPLITLPIWAH-VAVTALRFRITVCGIVTCWFLAGLSLPEFFFH 211
 Qy 120 YHIGYFGGIPPIIILIDRYLAIHVAFALKRTVFGVTSVITWLVAVEASVPIIIFT 179
 Db 152 CYMSLYSQFCITLILITVDRLLAVVAKVIMSLILPLIMAVYYVIRRLR-RPS 270
 Qy 180 KCQKEDSVVYCGYFPP---RGWNNFHTIMRNLTGFLPLIMVYCGYSGLKTLLRCNE 235
 Db 212 GHQDDNGRVQCDPYPTEMSTNVWRRAHVAKVIMSLILPLIMAVYYVIRRLR-RPS 270
 Qy 236 KKRRHRAVRVIFTIMIVYELFWTPYVNLVILLNTFQEFFGLSNCESTSQDOATQVTETLGM 295
 Db 271 KKCYKARLFLIVMVAYFWTPYVNLVILLSTFHATLNLQCALSNLDMLALITKTVAY 330

Qy	296 THCCINPIIYAFGEKFRRLSVPFRKHTIKRFECKQCP 333 Db 331 THCCINPVIYAFGEKFRRLYHFFHTVAYILCKYIP 368
RESULT 11	
Qy I49340	MIP-1 alpha receptor like-1 - mouse
C;Species: Mus musculus (house mouse)	
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004	
C;Accession: I49340	
R;Gao, J. L.; Murphy, P.M.	
J. Biol. Chem. 270, 17444-17501, 1995	
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine genes	
A;Reference number: I49339; MUID:9534046; PMID:7542241	
A;Accession: I49340	
A;Molecule type: DNA	
A;Cross-references: UNIPROT:P51676; EMBL:U28405; NID:9881549; PIDN:AAA89154.1; PMID:98815	
C;Superfamily: vertebrate rhodopsin	
Query Match Score 41.0%; DB 2; Length 356;	
Best Local Similarity 45.2%; Pred. No. 1.1e-59;	
Matches 154; Conservative 62; Mismatches 118; Indels 7; Gaps 4;	
Qy 25 DYDYGAPCHKEPKDVQKGQAQLPLPLSVPFGVFNMLVLLINCKLKULKCLTDYLNL 84 Db 18 DFMSGLCFSINVRAAGITVPTPLSVFPIGVTHVLQKRRNMTSYLFNL 77	
Qy 85 AISDLFLITLPLWA-HSAANNEWFGNAMCKLFTGMYHGICFGGIFTLTLTIDRYLATY 143 Db 78 AISDLFLSTLPLWFWDYIMGRDWFVNAMCKPVSFTSYLQLYSLSDNHFITLTIDRYLAVV 137	
Qy 144 HAVPAALKARTTIFGOTTSVITWLVAVPASVGLIIVTCQEDSVYVCGPYFPR---GNN 199 Db 138 HVVEFLARPARTVFGLISSITIWLLALVSPCLTYEKSOMEFTYTICRAILPRESLIRFL 197	
Qy 200 NFHTIRNLLGIVPLPLIMIVCYSGLKLTKLRCMEKGRARRVYIFTIMIVYFWTPY 259 Db 198 RFAQKTMNLLIPLLAMI CYTRVNRVHLR-RNKKEAKVVMRIFVTFITLFFLLAPY 256	
Qy 260 NIVLIVTQEFQFGNSNCESTSQSDQATOVTETLGNTHCCINPIIYAFKFRYLYSF 319 Db 257 YLAFFVSAFEDLFTPSCLRSQQVDSLMIETALAYTHCCVNPIVVFVGKRFRTKLWQL 316	
Qy 320 FRKHITKFRCKQCPVYRETDGTTSTNPSTQEVSAGL 360 Db 317 FRRHTAITLPLWLP-FLSEDRAQRSARLPSTVELETSADL 356	
RESULT 12	
Qy JC5067	G protein-coupled receptor CCR-L1 - human
N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6	
C;Species: Homo sapiens (man)	
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004	
C;Accession: JC5067; GO2276; GO2387	
R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.	
Biochem. Biophys. Res. Commun. 227, 846-853, 1996	
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like g	
A;Reference number: JC5067; MUID:97040707; PMID:8886020	
A;Accession: JC5067	
A;Molecule type: DNA	
A;Residues: 1-355 <ZAB>	
A;Cross-references: UNIPROT:P51685; EMBL:279782; NID:9166875; PIDN:CB02142.1; PID:9166	
R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.	
Submitted to the EMBL Data Library, June 1996	
A;Reference number: H01714	
A;Accession: GO2276	
A;Status: translated from GB/EMBL/DDBJ	
A;Molecule type: DNA	

Best Local Similarity 46.2%; Pred. No. 7.4e-55;	Db	126 DRYLAIVLAANSMNNRTVQHGVTTISLGWAAAAILVVAAPQFMEFK-QKENE--CLGDYPE 181
Matches 160; Conservative 46; Mismatches 121; Indels 19; Gaps 8;	Qy	197 GNNFTIMRN---LGLVPLLINVICYSGILKTLLRCNEKKRHRRAVRVIFTMIVY 252
24 PFDYGA-PCHRDVKQAGQLPPLSVFEGFVNMLWLLNCKLRLTDIYL 82	Db	182 VLOEINPVLNVETNFYFGELPLLINVICYSFRIQTLFSCKNHKA-KAIKLILLVVIP 240
13 PEYDDSAEACYLGDIVAFGTIFLSIPLSVLTFGLVGNLVLALTNSRSKSITDIYL 72	Qy	253 FLFWTPNIVILINTFOEFFGSNCESTSOLIDQATOVTETLGMTTHCCINPIIYAFGEKF 312
83 NDIAISDILFLITLPLWAHSAAANEWVFGNAMCMLKFTGLHYHGYFGGIFFFLTLTIDRYLA 142	Db	241 FLFWTPNVMFLETKLKYDPFPSCMRKDRLALSIVTAFSHCCLNPLIYAFGEKF 300
73 NDASDILFLATLPFWHLYLISHEGLINAMCMLTATTFFGFGGIFTIVTISIDRYLA 132	Qy	313 RRYLSTYFRK 322
143 VHAPALKARTVTFGVUTSITWLAVFASVPGIIFKQOKEDSDSVVTCGPYPGRGMNNFH 202	Db	301 RRYLYXLYGK 310
133 VLAANSKNNRTVQHGTISLGWAAAILVVASQFMEFK-RKDNE---CLGDYPEVLEQEIN 188		
Qy		RESULT 15
203 TIMR---NLIGLVLPLLINVICYSGILKTLLRCNEKKRRAVRVIFTMIVYFLFWTP 258	QC	JC5942 chemokine receptor - human
189 PVLRNSEVNLGFVPLPLIMSCYPRVLTFSCKNHKA-RAIRLILVVVFFLFWTP 247	C;Species: Homo sapiens (man)	C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
259 YNIVLILNTFOEFFGSNCESTSOLIDQATOVTETLGMTTHCCINPIIYAFGEKFPRRYLSV 318	C;Accession: JC5942	C;Accession: JC5942
248 YNIVLFLTSLTKEYNFFPSGMKRDLWALSVTETVAFSHCCLNPFYAFAGEKFKPRYLH 307	Db	R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
319 PFRKHITKRFCKQCPVY-----YRETVDGUTSTMTSPTEQEVSV 357	Qy	Biochem. Biophys. Res. Commun. 243, 264-268, 1998
308 LYNKCLAV-LGCR-PVHAGFSTESQRSRQDSLSSLTHYTSSEGEGS 351	Db	A;Title: Cloning and characterization of a novel human chemokine receptor.
		A;Reference number: JCS942; PMID:98139902; PMID:973515
		A;Accession: JC5942
		A;Status: preliminary
		A;Molecule type: DNA
		A;Residues: 1-344 <PAN>
		A;Cross-references: UNIPROT:000421; GB:U97123; NID:92897070; PID: AAC39595.1; PMID:928970:
		C;Superfamily: vertebrate rhodopsin
RESUL 14		
JC4304	Query Match	34.2%; Score 649.5; DB 2; Length 344;
orphan G protein-coupled receptor - human	Best Local Similarity 43.0%; Pred. No. 1.4e-48;	
N;Alternate names: V28 protein	Mismatches 54; Gaps 5;	
C;Species: Homo sapiens (man)	Matches 128; Conservative 128;	
C;Accession: JC4304	Query Match	27 DYGAPCHKFDYKQIGAQLLPPPLSVLFIPEGVGNMILVVLINCKLKCLTDIYLNLAI 86
R;Report, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.	Best Local Similarity 43.0%; Pred. No. 1.4e-48;	
Gene 163, 295-399, 1995	Mismatches 99; Gaps 99;	
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to 9	Db	23 DEAEQCDKIDQAQLSQQVBLCSAVFVGVDNLNLVLLVVKYKLKVNTNLNLAV 82
A;Reference number: JC4304; PMID:96011651; PMID:7590284	Qy	87 SDLLFLITLPLWAHSAAANEWVGNAMCMLKFTGLHYHGYFGGIFFFLLTIDRYLAHV-A 145
A;Molecule type: mRNA	Db	83 SNLCFLITLPEWAHG----GDPMKCLLIGLYPGLYSETFFNCLLTVORYLVFLHKG 136
A;Residues: 1-355 <RAP>	Qy	146 VPALKARTVTFGVUTSITWLAVFASVPGIILFTKCKQKEDSVYVCG---PYPPRG---W 198
Cross-references: UNIPROT:PA923B; GB:U20350; NID:g665580; PID:AAA91783.1;	Db	137 NFFSARRRVPFCGITISVLANVTAIATLPVYVVKQEMEDOKYKCFSRIPPLPADETFW 196
A;Experimental source: peripheral blood mononuclear cell	Qy	199 NNFTHTIMRNNTLGLVPLLINVICYSGILKTLLRCNEKKRRAVRVIFTMIVYFLWTPT 258
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals	Db	197 KHFLTKMNTSVLVLFITFLFLYQMRKTL--REFREQYSLFKVFAIRVFLNMWAP 253
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and	Qy	259 YNIVLILNTFOEFFGSNCESTSOLIDQATOVTETLGMTTHCCINPIIYAFGEKFRRYL 316
A;Gene: v28	Db	254 YNIAFFLSTPKHFSSDKCSSYNIDKSVHITKLJATTHCCINPIIYAFLDGTFSTYK 311
C;Superfamily: vertebrate rhodopsin		
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein		
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F;104-125/Domain: transmembrane #status predicted <TM2>		
F;146-165/Domain: transmembrane #status predicted <TM3>		
F;197-217/Domain: transmembrane #status predicted <TM4>		
F;230-254/Domain: transmembrane #status predicted <TM5>		
F;275-296/Domain: transmembrane #status predicted <TM7>		
Query Match	37.3%; Score 708; DB 2; Length 355;	
Best Local Similarity 46.8%; Pred. No. 1.3e-53;		
Matches 145; Conservative 47; Mismatches 108; Indels 10; Gaps 5;		
18 BEVTFEDY-DYGAPCHKFDYKQIGAQLLPPPLSVLFIPEGVGNMILVVLINCKLKCL 76	Qy	77 TDIVLNLAIASDLDLFLITLPLWAHSAAANEWVGNAMCMLKFTGLHYHGYFGGIFFFLLT
6 ESVTFENFEYDDLAECYTGIDIVFVTVFLSIFSVFAIGVGNLNUVFLNTNSKPKSY 65	Db	66 TDIYLNLAIASDLDLFLVATLPFWHLYLNEKGSLHNRACKFTTAFFPFGFESSIFFTVI 125
137 DRYLAIVHVAWSKAKARTVTFGVUTSITWLAVFASVPGIIFTKCKQEDSVYVCSPYFPR 196	Qy	

Search completed: June 9, 2005, 16:49:04
Job time : 27.0136 secs

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Scoring table:	BLOSUM62	Alignments		
Gapop 10.0 , Gapext 0.5				
Searched:	1612378 seqs, 512079187 residues			
Total number of hits satisfying chosen parameters:	1612378			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing:	Minimum Match 0% Maximum Match 100%			
	Listing first 45 summaries			
Database :	UniProt_03: 1: uniprot_sprot;* 2: uniprot_trembl;*			
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Query Score	Match Length	DB ID	Description
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
1	184.5	97.1	360	1 CKR2_MACMU
2	1651.5	86.9	374	1 CKR2_MACMU
3	1542	81.2	373	1 CKR2_RAT
4	5	80.8	373	1 CKR2_MOUSE
5	1513	79.6	373	1 Q6YT42
6	1403	73.8	354	2 Q66G28
7	1396	73.5	354	1 CKR5_MOUSE
8	1392	73.3	352	2 Q95NC2
9	1386	72.9	354	1 CKR5_RAT
10	1383	72.8	352	1 CKR5_RAT
11	1377	72.5	352	2 Q6RN96
12	1376	72.4	352	1 CKR5_CERTO
13	1376	72.4	352	2 Q71RS2
14	1375	72.4	352	2 Q77756
15	1375	72.4	352	2 Q8HZT9
16	16	72.4	352	2 Q9mza
17	1374	72.3	352	2 Q6RN98
18	1373	72.3	352	2 Q95NE1
19	1373	72.3	352	2 Q6WN93
20	1371	72.2	352	1 CKR5_HYLLE
21	1371	72.2	352	2 Q95NC4
22	1371	72.2	352	2 Q95NC9
23	1371	72.2	352	2 Q6RN97
24	1371	72.2	352	2 Q9xt12
25	1370	72.1	352	1 CKR5_MACMU
26	1370	72.1	352	1 CKR5_MACMU
27	1370	72.1	352	1 CKR5_MACMU
28	1370	72.1	352	1 CKR5_PANPA
29	1370	72.1	352	1 CKR5_PANTR
30	1370	72.1	352	1 CKR5_PONPA
31	1370	72.1	352	1 CKR5_PONY
32	1370	72.1	352	2 Q71TT22
33	1370	72.1	352	2 Q71TT27
34	1370	72.1	352	2 Q71TT28
35	1370	72.1	352	2 Q71TT29
36	1368	72.0	352	1 CKR5_GORGO
37	1368	72.0	352	1 CKR5_LOPAT
38	1368	72.0	352	1 CKR5_PAPAN
39	1368	72.0	352	1 CKR5_PAFA
40	1368	72.0	352	1 CKR5_PAFA
41	1368	72.0	352	2 Q6WN92
42	1368	72.0	352	2 Q6WN94
43	1368	72.0	352	2 Q71TT20
44	1368	72.0	352	2 Q71TT21
45	1368	72.0	352	2 Q71UI8

PT DOMAIN 71 80 Cytoplasmic (Potential).
PT TRANSMEM 81 100 2 (Potential).
PT DOMAIN 101 114 Extracellular (Potential).
PT TRANSMEM 115 136 3 (Potential).
PT DOMAIN 137 153 Cytoplasmic (Potential).
PT TRANSMEM 154 178 4 (Potential).
PT DOMAIN 179 206 Extracellular (Potential).
PT TRANSMEM 207 226 5 (Potential).
PT DOMAIN 227 243 Cytoplasmic (Potential).
PT TRANSMEM 244 268 6 (Potential).
PT DOMAIN 269 285 Extracellular (Potential).
PT TRANSMEM 286 309 7 (Potential).
PT DOMAIN 310 360 Cytoplasmic (Potential).
PT CARBOHYD 14 14 N-linked (GlcNAc, .). (Potential).
MOD RES 26 26 Sulfotyrosine (By similarity).
FT DISTIDF 113 190 By similarity.
SEQUENCE 360 AA; 41139 MW; 4B2552BC913FB9P CRC64;

Query Match 97.1%; Score 1845; DB 1; Length 360;
Best Local Similarity 96.9%; Pred. No. 5 1e-106;
Matches 349; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MLTSRSRFIRNTNNGEETTFFDYGACHKPDYKQIGAQQLPPLYSLVVFIFGVEN 60
Db 1 MLTSRSRFIRNTNNGEETTFFDYGACHKPDYKQIGAQQLPPLYSLVVFIFGVEN 60
Qy 61 MLLVLLINCKDKLCLDIYLNLASDLLELTPLWAAANNEWFGNAMCKLFTGLY 120
Db 61 MLLVLLINCKDKLCLDIYLNLASDLLELTPLWAAANNEWFGNAMCKLFTGLY 120
Qy 121 HIGYFGGILFILLTIDRYLAIVHAYFALKARTVTFGVVTSVITLVAVASVPGIIFTK 180
Db 121 HIGYLGILFILLTIDRYLAIVHAYFALKARTVTFGVVTSVITLVAVASVPGIIFTK 180
Qy 181 CQEDSYVVCGPYFPGRQWNPFNTIMENILGLYPLIMIVCYSGILKTLLRCNEKRRH 240
Db 181 CQEDSYVVCGPYFPGRQWNPFNTIMENILGLYPLIMIVCYSGILKTLLRCNEKRRH 240
Qy 241 AYVIFTMIVFLFWTPNIVLNLNTFQFFGLSNCESTSQLDQTQTVTTLGTMHCCI 300
Db 241 AYVLFITMIVFLFWTPNIVLNLNTFQFFGLSNCESTSQLDQTQTVTTLGTMHCCI 300
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Db 301 NPIIYAFVGKEPRYLSSVFRGHITKRFCQKCPVFTRTDVGTSTNTPSTGEQVSYAGL 360
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=3606;

RESULT 2
CKR2_HUMAN STANDARD; PRT; 374 AA.

AC P41597; 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=3606;

RN SEQUENCE FROM N.A.; PubMed=8146186;
RN MEDLINE=94195821; Charo I.F., Myers S.J., Herman A., Connolly A.J., Coughlin S.R.; "Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternative splicing of the carboxyl-terminal tail." RT
RN Proc. Natl. Acad. Sci. U.S.A., 91:2752-2756 (1994).
RN SEQUENCE FROM N.A.; PubMed=8048929;
RN MEDLINE=94324942;

DR	GO; GO:0005887; C:integral to plasma membrane; TAS.	301. NPIIYAFVGKFR--SLP--HIAAG-CRIAPL 327
DR	GO; GO:000625; C:soluble fraction; TAS.	
DR	GO; GO:000950; F:chemokine receptor activity; TAS.	
DR	GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .); TAS.	
DR	GO; GO:0006968; P:cellular defense response; TAS.	
DR	GO; GO:0008935; P:chemotaxis; TAS.	
DR	GO; GO:0007204; P:cyclosolic calcium ion concentration elevation; TAS.	
DR	GO; GO:0006954; P:inflammatory response; TAS.	
DR	GO; GO:0007259; P:JAK-STAT cascade; TAS.	
DR	GO; GO:0019194; P:negative regulation of adenylyl cyclase ac. . .; TAS.	
DR	INTERPRO; IPR002237 CC_2 receptor.	
DR	INTERPRO; IPR00355; Chk1-like receptor.	
DR	INTERPRO; IPR00276; GPCR_Rhodpsn.	
DR	Pfam; PF00001; 7tm_1; 1.	
DR	PRINTS; PRO0237; GPCRHODOPSN.	
DR	PROSITE; PS50262; G PROTEIN RECEPTOR_F1.2; 1.	
KW	3D-structure; Alternative splicing; G-protein coupled receptor;	
KW	Glycoprotein; Polymorphism; Transmembrane.	
FT DOMAIN	1 42	Extracellular (Potential).
PT TRANSMEM	43 70	1 (Potential).
PT DOMAIN	71 80	Cyttoplasmic (Potential).
PT TRANSMEM	81 100	2 (Potential).
PT DOMAIN	101 114	Extracellular (Potential).
PT TRANSMEM	115 136	3 (Potential).
PT DOMAIN	137 153	Cyttoplasmic (Potential).
PT TRANSMEM	154 178	4 (Potential).
PT DOMAIN	179 206	Extracellular (Potential).
PT TRANSMEM	207 226	5 (Potential).
PT DOMAIN	227 243	Cyttoplasmic (Potential).
PT TRANSMEM	244 269	6 (Potential).
PT DOMAIN	269 285	Extracellular (Potential).
PT TRANSMEM	286 309	7 (Potential).
PT DOMAIN	310 374	Cyttoplasmic (Potential).
PT CARBOHYD	14 14	N-linked (GlcNAc. . .) (Potential).
PT MOD_RES	26 26	Sulfotyrosine.
PT DISURID	113 190	By similarity.
PT VARSPLIC	314 374	SLFHIALGCRAPLQPKVCGGPVGRPGKNVKVTGGLDDR CGKGSIGRAPASLQDKEGA --> RYLSPFTRKHTIKRPK QCPVPTRTBTQGVTSNTPTSGEQEVSGAL (in isoform B).
FT FTID=VSP_001893.		
FT VARIANT	64 64	V -> I (in dbsnp_1.1799864).
FT VARIANT	355 355	/FTID=AVAR_014339.
FT VARIANT		G > E.
FT SEQUENCE	374 AA; 41914 MW; F865B0D3B74CFC0F CRC64;	/FTID=VAR_014340.
Query Match	86.3%; Score 1651.5;	DB 1; Length 374;
Best Local Similarity	95.5%; Pred. No. 4.2e-94;	
Matches	319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;	
Qy	1 MLSTSRSRFIRNTNESEBEYTFPDYDGAPCHKFDPYKQIGAQQLPPLYSLVFIFGVGN 60	
Db	1 MLSTSRSRFIRNTNESEBEYTFPDYDGAPCHKFDPYKQIGAQQLPPLYSLVFIFGVGN 60	
Qy	61 MLVVLILINKKLKCUTDIYLNLASDLFLITPLWAISAAANTVFGNAMCKLFITGLY 120	
Db	61 MLVVLILINKKLKCUTDIYLNLASDLFLITPLWAISAAANTVFGNAMCKLFITGLY 120	
Qy	121 HIGYFGGIFFILLTIDRYLAVIHAYFALKARTVTPGVVSVITLVAVASPGLIFTK 180	
Db	121 HIGYFGGIFFILLTIDRYLAVIHAYFALKARTVTPGVVSVITLVAVASPGLIFTK 180	
Qy	181 CQEDSVYCCGPYFPGRWNPHITMENILGLVPLIMIVCYSGILKTLLRCNEKRRHR 240	
Db	181 CQEDSVYCCGPYFPGRWNPHITMENILGLVPLIMIVCYSGILKTLLRCNEKRRHR 240	
Qy	241 AVRVITMMITYPLFTPTVYVILLANTFOEFGLSNCESTSOLDQATQVETLGTHCC 300	
Db	241 AVRVITMMITYPLFTPTVYVILLANTFOEFGLSNCESTSOLDQATQVETLGTHCC 300	
Qy	301 NPIIYAFVGKFRKFRHITRKFCIQCPV 334	
DR	SEQUENCE 374 AA; 41914 MW; F865B0D3B74CFC0F CRC64;	81.2%; score 1542; DB 1; Length 373;

QY	Best Local Similarity 80.0%; Pred. No. 2.3e-87; Matches 248; Conservative 24; Mismatches 48;	Indels 0; Gaps 0;	-1 - SUBCELLULAR LOCATION: Integral membrane protein.
Db	1 MLSTSRSPFRTNTNEGEETTFFDYGAPCCKEDPKVQIQAQLPPLSVPFLFGFVN 60	CC -1 TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines, but not in nonhematopoietic cell lines.	
Db	14 ILSTSHSLPPRSIQELDEGATTPYDDEGPCKHTSVKQIGAWLPLPSLVPFLFGFVN 73	CC -1 SIMILARITY: Belongs to the G-protein coupled receptor 1 family.	
QY	61 MLVYLILINGKKLKCLDTIYLNLAIISDLFLITLPLWAHAAANEWVFGNAMCKLFITLY 120	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
Db	74 MLVYLISCKLKSMTDIYLNALISDLFLITLPLWAHAAANEWVFGNAMCKLFITGY 133	CC	
QY	121 HIGYFGGIFTPLLTIDRYLAIVHVAFLKARTTFGVVTSVITWLVAFAVGIIIFIK 180	CC	
Db	134 HIGYFGGIFTPLLTIDRYLAIVHVAFLKARTTFGVVTSVITWLVAFAVGIIIFIK 193	CC	
QY	181 CQKEDSVVYCGPYPPRGWMNHFIMRNLLGVLVPLIMIVCYSGILKTLRCKNEKKHR 240	CC DR EMBL; USL17; AAC52453.1; -.	
Db	194 SEQEDQHTCGPYFPPTWTKWQFTIMRNLLSILPLVMIVCYSGILHTLFRCRNEKKHR 253	CC DR EMBL; USL19; AAC52784.1; -.	
QY	241 AVRIFTIMIVYFLWMPWTPNIVLANTQFFGLSNCESTSOLQDQATOVTETGMTHCJ 300	CC DR MGD; MGI-106385; PIC-C chemokine receptor activity; IDA.	
Db	254 AVERLPAIMIVYFLWMPWTPNIVLANTQFFGLSNCESTSOLQDQATOVTETGMTHCJ 313	CC DR GO:0016493; Fc cytokine binding; IPI.	
QY	301 NPITYAFVGKFRYRLSVFPRKHITRKFCQCPVYRFETDGVTSTNTPTGEQVSAGL 360	CC DR GO:0019955; P-cellular defense response (sensu Vertebrata); IMP.	
Db	314 NPITYAFVGKFRYRLSVFPRKHITRKFCQCPVYRFETDGVTSTNTPTGEQVSAGL 373	CC DR GO:0006954; P-humoral immune response; IMP.	
RESLT 4	CKR2_MOUSE STANDARD; PRT; 373 AA.	CC DR GO:0019233; P-inflammatory response; IMP.	
ID	P51633; Q61172;	CC DR GO:0030334; P-perception of pain; IMP.	
AC	01-OCT-1995 (Rel. 34, Created)	CC DR InterPro; IPR002231; P-regulation of cell migration; IMP.	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	CC DR InterPro; IPR000355; CC 2 receptor.	
DT	25-OCT-2004 (Rel. 45, Last annotation update)	CC DR InterPro; IPR000276; GPCR_7tm1_1.	
DE	C-C chemokine receptor type 2 (C-C CCR-2) (CCR-2) (CCR2)	CC DR PRINTS; PR00237; GCRRHODOPEN.	
DE	(JE/FIC receptor) (MCP-1 receptor).	CC DR PROSITE; PS00237; G PROTEIN RECEPTOR_1_1; 1.	
GN	Name=cckr2; Synonyms=cckbx2;	CC DR PROSTE; PS50262; G PROTEIN RECEPTOR_F1_2; 1.	
OS	Mus musculus (Mouse)	CC DR KW G-protein coupled receptor; Transmembrane, Extracellular (Potential).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	CC DR FT DOMAIN 1 55 1 (Potential).	
OX	NCBI_TaxID-10090; [1]	CC DR FT DOMAIN 1 56 83 1 Cytoplasmic (Potential).	
RN	SEQUENCE FROM N.A.	CC DR FT DOMAIN 1 57 93 2 (Potential).	
RP	RP MEDLINE#96205938; PubMed#8631787; DOI=10.1074/jbc.271.13.7551; RX Boring L., Gosling J., Monteciaro F.S., Luisi A.J., Tsou C.-L., RA Charo I.F.; RT "Molecular cloning and functional expression of murine JE (monocyte RA chemoattractant protein 1) and murine macrophage inflammatory protein RT alpha receptors: evidence for two closely linked C-C chemokine RT receptors on chromosome 9"; RT RT receptors on chromosome 9"; RT RT RT RT RT RN [2] SEQUENCE FROM N.A. RP STRAIN-BALB/C; MEDLINE#9616064; PubMed#8662823; DOI=10.1074/jbc.271.20.11603; RX Kurihara T., Bravo R.; RT "Cloning and functional expression of mCCR2, a murine receptor for the RT C-C chemokines JE and FIC." ; RT RT RN [3] SEQUENCE FROM N.A. RP MEDLINE#97026720; PubMed#8872898; DOI=10.1002/(SICI)1097-4547(19960815)45:4<382::AID-JNR7>3.3.CO;2-H; RX Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R., RL J. Biol. Chem. 271:11603-11606 (1996). RN	CC DR FT DOMAIN 1 58 94 3 (Potential).	
QY	1 MLSTSRSPFRTNTNEGEETTFFDYGAPCCKEDPKVQIQAQLPPLSVPFLFGFVN 60	CC DR FT DOMAIN 1 59 127 3 Cytoplasmic (Potential).	
Db	14 IUSTSHSLPPRSIQELDEGATTPYDDEGPCKHTSVKQIGAWLPLPSLVPFLFGFVN 73	CC DR FT DOMAIN 1 60 128 149 3 (Potential).	
QY	61 MLVYLILINGKKLKCLDTIYLNLAIISDLFLITLPLWAHAAANEWVFGNAMCKLFITGLY 120	CC DR FT DOMAIN 1 61 150 166 4 (Potential).	
Db	74 MLVYLISCKLKSMTDIYLNALISDLFLITLPLWAHAAANEWVFGNAMCKLFITGY 133	CC DR FT DOMAIN 1 62 167 191 4 (Potential).	
QY	121 HIGYFGGIFTPLLTIDRYLAIVHVAFLKARTTFGVVTSVITWLVAFAVGIIIFIK 180	CC DR FT DOMAIN 1 63 192 219 5 (Potential).	
Db	134 HIGYFGGIFTPLLTIDRYLAIVHVAFLKARTTFGVVTSVITWLVAFAVGIIIFIK 193	CC DR FT DOMAIN 1 64 220 239 5 (Potential).	
QY	181 COREDSYYVCGPYFPGWNPHTIMENILGLVPLIMVICGSIKLTLRCKNEKKHR 240	CC DR FT DOMAIN 1 65 240 256 6 (Potential).	
Db	194 SKQDDHYTCGPFQTMWNQFOTIMENILSLPLVMVICGSIKLTLRCKNEKKHR 253	CC DR FT DOMAIN 1 66 257 281 6 (Potential).	
QY	Best Local Similarity 80.6%; Score 1535; DB 1; Length 373;	CC DR FT DOMAIN 1 67 282 298 7 (Potential).	
Matches 287; Conservative 25; Mismatches 48; Indels 0; Gaps 0;	CC DR FT DOMAIN 1 68 299 322 7 (Potential).		
Db	Query Match 1 MLSTSRSPFRTNTNEGEETTFFDYGAPCCKEDPKVQIQAQLPPLSVPFLFGFVN 60	CC DR FT DOMAIN 1 69 323 373 7 (Potential).	
QY	14 IUSTSHSLPPRSIQELDEGATTPYDDEGPCKHTSVKQIGAWLPLPSLVPFLFGFVN 73	CC DR FT DOMAIN 1 70 374 42782 MW; EA012C10F4C9325A CRC64;	
QY	SEQUENCE FROM N.A. RP STRAIN-BALB/C; MEDLINE#9616064; PubMed#8662823; DOI=10.1074/jbc.271.20.11603; RX Kurihara T., Bravo R.; RT "Cloning and functional expression of mCCR2, a murine receptor for the RT C-C chemokines JE and FIC." ; RT RT RN [3] SEQUENCE FROM N.A. RP MEDLINE#97026720; PubMed#8872898; DOI=10.1002/(SICI)1097-4547(19960815)45:4<382::AID-JNR7>3.3.CO;2-H; RX Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R., RL J. Biol. Chem. 271:11603-11606 (1996). RN	CC DR FT DOMAIN 1 71 42782 MW; EA012C10F4C9325A CRC64;	
QY	SEQUENCE FROM N.A. RP STRAIN-BALB/C; MEDLINE#9616064; PubMed#8662823; DOI=10.1074/jbc.271.20.11603; RX Kurihara T., Bravo R.; RT "Cloning and functional expression of mCCR2, a murine receptor for the RT C-C chemokines JE and FIC." ; RT RT RN [3] SEQUENCE FROM N.A. RP MEDLINE#97026720; PubMed#8872898; DOI=10.1002/(SICI)1097-4547(19960815)45:4<382::AID-JNR7>3.3.CO;2-H; RX Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R., RL J. Biol. Chem. 271:11603-11606 (1996). RN	CC DR FT DOMAIN 1 72 42782 MW; EA012C10F4C9325A CRC64;	
QY	1 MLVYLILINGKKLKCLDTIYLNLAIISDLFLITLPLWAHAAANEWVFGNAMCKLFITGLY 120	CC DR FT DOMAIN 1 73 42782 MW; EA012C10F4C9325A CRC64;	
Db	74 MLVYLISCKLKSMTDIYLNALISDLFLITLPLWAHAAANEWVFGNAMCKLFITGY 133	CC DR FT DOMAIN 1 74 42782 MW; EA012C10F4C9325A CRC64;	
QY	121 HIGYFGGIFTPLLTIDRYLAIVHVAFLKARTTFGVVTSVITWLVAFAVGIIIFIK 180	CC DR FT DOMAIN 1 75 42782 MW; EA012C10F4C9325A CRC64;	
Db	134 HIGYFGGIFTPLLTIDRYLAIVHVAFLKARTTFGVVTSVITWLVAFAVGIIIFIK 193	CC DR FT DOMAIN 1 76 42782 MW; EA012C10F4C9325A CRC64;	

Matches	264;	Conservative	30;	Mismatches	50;	Indels	6;	Gaps	2;
Qy	17	GEETTPFFDDY--GAPCHFDFVKOIGAQOLPPPLSVPTFGVGNMLVVLINCKLK	74						
Db	5	GSIPYYIDYDSMSPAPCPNVIQIAAQOLPPPLSVPTFGVGNMLVVLISCKLK	64						
Qy	75	CLTDIYLLNAISDLFLTLTLPWAHSAAANEWVCPNVIQIAAQOLPPPLSVPTFGVGNMLVVLISCKLK	134						
Db	65	SMTDIYLNIAISDLFLTLTLPWAHYAANEWVCPNVIQIAAQOLPPPLSVPTFGVGNMLVVLISCKLK	124						
Qy	135	TIDRYLAVIAHVAFALKARTTGFVUTSVITWLVAFAASVGLIIFTKQCQBDSTYVCGYP	194						
Db	125	TIDRYLAVIAHVAFALKARTTGFVUTSVITWLVAFAASVGLIIFTKQCQBDSTYVCGYP	184						
Qy	195	P---RGWNNFTIPTNLGVLPLVLMTCYSGILKTLLRCRNEKRRARVIFTMI	250						
Db	185	PRIQTRFWKHQTQLKVNLSLPLPVWVTCYSGILNTLRCRNEKRRARVLFAIM	244						
Qy	251	VPLEFTPTVNVILLNTFOREFFGLSNCEBTSQSDQATOATVETLGMTHCCNPIIYAFGE	310						
Db	245	VPLEFTPTVNVILLNTFOREFFGLSNCEBTSQSDQATOATVETLGMTHCCNPIIYAFGE	304						
Qy	311	KFRVNLSPVPRKHITKRPCKOCVPVFRTETDGVTSINTPTEQEVSAGI	360						
Db	305	KFRVNLSPVPRKHITKRPCKOCVPVFRTETDGVTSINTPTEQEVSAGI	354						

RESULT 7

Ckrs5 - MOUSE

ID Ckrs5 MOUSE STANDARD; PRT; 354 AA.
AC P51632; 035312; 035891; P97308; P97405; Q61867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)

DB C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
alpha receptor).

DE Name=Ccr5; Synonyms=Cmkbs5;

OS Mus musculus (Mouse);
OC Metazoa; Chordata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NCBI_TaxID:10090;

RN SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Spleen; RT
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus; RT
RX MEDLINE=96278910; PubMed=86628920; DOI=10.1074/jbc.271.24.14445;
RA Meyer A., Coyle A.J., Proudfoot A.B.I., Wells T.N.C., Power C.A.,
RA Charo I.F.; "Cloning and characterization of a novel murine macrophage
RT chemotactrant protein-1 and murine macrophage inflammatory protein
RT 1alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9.";
RT J. Biol. Chem. 271:7551-7558 (1996).
RL

[2] RT
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus; RT
RX MEDLINE=96278910; PubMed=86628920; DOI=10.1074/jbc.271.24.14445;
RA Meyer A., Coyle A.J., Proudfoot A.B.I., Wells T.N.C., Power C.A.,
RA Charo I.F.; "Cloning and characterization of a novel murine macrophage
RT inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 271:14445-14451 (1996).
RN [3]
RN SEQUENCE FROM N.A.
RC Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.,
RN Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.

[4] RT
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
RX Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RA "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses."

RL J. Virol. 71:8642-8655 (1997).

[5] RN
SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=97404635; PubMed=9261347;
RA Doran B.J., Lu Z.H., Rucker J.J., Zhang T.Y., Sharron M., Cen Y.H.,
RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;

"Two distinct CCR5 domains can mediate coreceptor usage by human
RT immunodeficiency virus type 1.";
J. Virol. 71:6305-6314 (1997).
[6]

RP
SEQUENCE FROM N.A.
RA Guo B., Kuno K., Harada A., Matsushima K.;

RA Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC but not in nonhematopoietic cell lines.
CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC
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CC

CC
DR EMBL U47036; AAC2454.1;
DR EMBL X94151; QAA63867.1;
DR EMBL U68565; AAB3723.1;
DR EMBL U83327; AAC53286.1;
DR EMBL AF022990; AAC53389.1;
DR EMBL AF019772; AAB120183.1;
DR EMBL DB364; BAA12024.1;
DR MGD; MGI:1071842; CC25.
DR GO; GO:0016493; F-C-C chemokine receptor activity; IDA.
DR GO; GO:0006952; p:defense response; IMP.
DR InterPro; IPR002240; CC_5 receptor.
DR InterPro; IPR000355; Chimidine receptor.
DR InterPro; IPR00276; GPCR_Rhodopsn.

CC
DR PFAM_P00001; 7tm_1.
DR PRINTS; PR00237; GPBRHRODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECPEP_F1_1;
DR PROSITE; PS50222; G-PROTEIN_RECPEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.

CC
DOMAIN 1 FT TRANSMEM 33 60 1 (Potential).
DOMAIN 1 FT TRANSMEM 61 70 2 (Potential).
FT TRANSMEM 71 91 Extracellular (Potential).
DOMAIN 92 104 3 (Potential).
FT TRANSMEM 105 126 4 (Potential).
FT TRANSMEM 127 143 5 (Potential).
FT TRANSMEM 144 168 6 (Potential).
FT TRANSMEM 169 200 7 (Potential).
FT TRANSMEM 201 220 Extracellular (Potential).
FT TRANSMEM 221 237 Cytoplasmic (Potential).
FT TRANSMEM 238 262 Extracellular (Potential).
FT TRANSMEM 263 279 Extracellular (Potential).
FT TRANSMEM 280 303 Cytoplasmic (Potential).
FT TRANSMEM 304 354 Cytoplasmic (Potential).
FT DISULPID 103 180 By similarity.
FT CARBOHYD 270 270 N-linked (GlcNAc. . .) (Potential).

CC
I -> S.
K -> R.
V -> M.
V -> L.
V -> A.
P -> S.
P -> L.

CC
I -> S.

FT	VARIANT	213	213	I -> V.	DR	PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.
FT	VARIANT	318	318	I -> M.	DR	PROSITE; PS00237; G-PROTEIN RECEPTOR-F1_1;-1.
FT	VARIANT	337	337	V -> A.	DR	PROSITE; PS00262; G-PROTEIN RECEPTOR-F1_2;-1.
FT	CONFLICT	3	3	F -> L (In Ref. 2).	KW	G-protein coupled receptor; Transmembrane.
FT	CONFLICT	80	80	L -> F (In Ref. 2).	SQ	SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;
FT	CONFLICT	145	145	N -> I (In Ref. 5).		
FT	CONFLICT	190	190	H -> Y (In Ref. 3).		
FT	CONFLICT	208	208	P -> S (In Ref. 1).		
SQ	SEQUENCE	354 AA;	40863 MW;	B4A6B942B889FC0 CRC64;		
	Query Match	73.5%	Score 1396; DB 1; Length 354;	DR	PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.	
	Best Local Similarity	74.6%	DB 1; Pred. No. 2.1e-78;	DR	PROSITE; PS00237; G-PROTEIN RECEPTOR-F1_1;-1.	
	Matches 261; Conservative 33; Mismatches 50; Indels 6; Gaps 2;		KW	G-protein coupled receptor; Transmembrane.		
Qy	17	GEEVTTPPDYDG-APCHKPDYKQIGQQLPPLSLYFIFGTGNMLVVLILINCKLK 74	DR	PROSITE; PS00262; G-PROTEIN RECEPTOR-F1_2;-1.		
Db	5	GSPVPTXYIDYDMSAPCKQINKYKQIAQQLLPPPLSYFIFGTGNMLVVLILISCKLK 64	SQ	SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;		
Qy	75	CIDIYLNLALASDLFLITLPIWAHSANNEWFGNAMCKLFTGTHIGYFGGIFFILL 134	DR	PROSITE; PS00237; G-PROTEIN RECEPTOR-F1_1;-1.		
Db	65	SVIDIYLNLALASDLFLITLPIWAHSANNEWFGNAMCKLFTGTHIGYFGGIFFILL 124	SQ	SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;		
Qy	135	TIDRYLAIVAHVAPALKARTTGFCSVTSVTIWLAVAFASVPGILTICSGILKTLRCRNEKEKHKRAVRVIFTIMIV 251	DR	PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.		
Db	125	TIDRYLAIVAHVAPALKARTTGFCSVTSVTIWLAVAFASVPGILTICSGILKTLRCRNEKEKHKRAVRVIFTIMIV 243	SQ	SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;		
Qy	195	PRG --- MNNEHTIMRLVILGLVPLLMIVCYSGLILTLLRCNEKEKRRAVRVIFTIMI 250	DR	PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.		
Db	185	PRQYHFWKSFQTLKMYVLLSLPLVWMCYCYSGLILTLLRCNEKEKRRAVRVIFTIMI 244	SQ	SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;		
Qy	251	VTFPLWTPTNVIVLNLNTFQEFFGLNSCCTSOLQDQATOVTETLGTMHCINPIIYAFVGK 310	DR	PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.		
Db	245	VTFPLWTPTNVIVLNLNTFQEFFGLNSCCTSOLQDQATOVTETLGTMHCINPIIYAFVGK 304	SQ	SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;		
Qy	311	KPFRRYLVSFVRKHITKPKOCVPFYRETVDGYTSNTPSTGEQEVSAGL 360	DR	PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.		
Db	305	KFRSRYLSVFRKHIVGKCFRKCSIFQQDNPDRVSSYTRSTGEHEVYSTGL 354	SQ	SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;		
	RESULT 9					
	CKR5_RAT					
	ID	CKR5_RAT				
	AC	008556;				
	DT	01-NOV-1997 (Rel. 35. Created)				
	DT	01-NOV-1997 (Rel. 35. Last sequence update)				
	DT	25-OCT-2004 (Rel. 45. Last annotation update)				
	DE	C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1 alpha receptor).				
	DS	Name=Cor5; Synonyms=Gmkb5;				
	GN	Rattus norvegicus (Rat).				
	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
	OC	NCBI_TaxID=10116;				
	RN	[1]_SEQUENCE FROM N.A.				
	RP	SEQUENCE FROM N.A.				
	RC	STRAIN=Wistar; TISSUE=Brain;				
	RX	MEDLINE=9833466; PubMed=9670989;				
	RX	DOI=10.1002/(SICI)1097-4547(19980701)53:1<16::AID-JNR3>3.0.CO;2-0;				
	RA	Spleiss O., Gourmalas N., Boddeke H.W.G.M., Sauter A., Fiebich B.L., Berger M., Gebicke-Haerter P.J.;				
	RT	"Chemokine receptor expression in cultured glia and rat experimental allergic encephalomyelitis".				
	RT	J. Neurosci. Res. 53:16-28(1998).				
	RN	[2]_SEQUENCE FROM N.A.				
	RC	STRAIN=Sprague-Dawley;				
	RX	MEDLINE=98318173; PubMed=9655467; DOI=10.1016/S0165-5728(98)00005-8;				
	RA	Jiang Y., Salaffraza M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., Debiec C.M., Pennell N.A., Streit W.J., Harrison J.K.;				
	RT	"Chemokine receptor expression in cultured glia and rat experimental allergic encephalomyelitis".				
	RT	J. Neuroimmunol. 86:1-12(1998).				
	CC	- - FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,				
	CC	MIP-1-beta and RANTES and subsequently transduces a signal by				
	CC	increasing the intracellular calcium ions level.				
	CC	- - SUBCELLULAR LOCATION: Integral membrane protein.				
	CC	- - SIMILARITY: Belongs to the G-protein coupled receptor 1 family.				

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DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DE	Chemokine (C-C motif) receptor 5 (Chemokine C-C motif receptor 5).		
GN	Name=CC5;		
OC	Sub_scorfa (Pig).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OC	NCBI_TaxID=9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H., Awata T., Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.		
RI	[2]		
RN	SEQUENCE FROM N.A.		
RA	Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H., Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.		
RL	[3]		
RN	SEQUENCE FROM N.A.		
RA	Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T., Uenishi H., Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.		
CC	-1 - SUBCELLULAR LOCATION: Integral membrane protein (By similarity).		
CC	-1 - SIMILARITY: Belongs to family 1 of G-protein coupled receptors.		
DR	EMBL; AP006185; BAD086491; -.		
DR	EMBL; AP006435; BAD086561; -.		
DR	EMBL; AB119272; BAD121351; -.		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0016493; F:chemokine receptor activity; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.		
DR	InterPro; IPR00923; BlueCu_1.		
DR	InterPro; IPR00240; CC_5_receptor.		
DR	InterPro; IPR00355; Chemkine receptor.		
DR	InterPro; IPR00276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00657; CCHEMOKINER.		
DR	PRINTS; PR1110; CHEMOKINERS.		
DR	PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.		
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.		
DR	PROSITE; PS00232; G_PROTEIN_RECEP_F1_2; 1.		
KW	G-protein coupled receptor; Receptor; Membrane.		
SQ	SEQUENCE 352 AA; 40227 MW; 74649B930911C987 CRC64;		
Query Match Score 72.8%; Best Local Similarity 74.5%; Matches 260; Conservative 33; Mismatches 50; Indels 6; Gaps 2;	Score 1383; DB 2; Length 352; Best Local Similarity 74.5%; Pred. No. 1..3e-77; Indels 6; Gaps 2;		
Y	17 GEEVTTFFDYD--GAPCHFHDVKOIGAQOLPPPLSVTFGFVGNMVLVLLINCKLK 74	Y	18 BBVTTFFDYD--APCHKFVDKQIGAQOLPPPLSVTFGFVGNMVLVLLINCKLK 75
Y	5 GSIPYYDDYNSAPCQVNVQIAQQPLPLSVLFPGFVGNMVMFLISCKLK 64	Y	4 QTTSPPYDIDYGMSEPCQKTNVRQARILPPPLSVTFGFVGNMVLVLLINCKLK 63
Y	75 CLTDYLNLAISDLEFLTLPLWAHSAANNEWFENAMCQLFTGLYHICGXFGGIFFFITL 134	Y	76 LTDIVLNLAISDLEFLTLPLWAHAAANNEWFENAMCQLFTGLYHICGXFGGIFFFITL 135
Y	65 SMTDYLFLNAISDLEFLTLPLFWAHYAAANNEWFENAMCQLFTGLYHICGXFGGIFFFITL 124	Db	64 MTDIVLNLAISDLEFLTLPTFWAHAAQMSQEGSHYTCSPHP 184
Y	135 TIDYLAIVAVAPALKARTTGFVTSVITWLVAFAASVGLIIFTKQKEDSDVTVCGPYF 194	Y	136 IDRYLAIVAHVFKARTTGFVVTTSVITWLVAFAASVGLIIFTKQKEDSDVTVCGPYFP 195
Y	125 TIDYLAIVAVAFKARTTNGVTSVITWLVAFAASVGLIIFTKQKEDSDVTVCGPYF 184	Y	124 IDRYLAIVAHVFKARTTGFVVTTSVITWLVAFAASVGLIIFTKQKEDSDVTVCGPYFP 183
Y	195 ---PRGWNFHFTMRNLTGVLPLLMITYCSIGLKLTLRCNEKKHRAYVIFTIMV 250	Y	196 RG---WNNFHTIMRNLTGVLPLLMITYCSIGLKLTLRCNEKKHRAYVIFTIMV 251
Y	185 LHIQYRFWKEHQTLKMLVLLSLPLLWVYCYSGLNLTRCRNEKKHRAYVRLFAIMI 244	Y	184 SSQYHFKNPFQTLKMLVLLSLPLLWVYCYSGLNLTRCRNEKKHRAYVRLFAIMI 243
Y	305 KFRRLSVFPRKHTTKRCKQCPVTPYRTVDGTSTNTPTGEQEVSTGL 354	Y	252 YFLFWTYNIVNLLSTQEFFGLSNCESTSQDQATOATVETLGMTHCCINPIYAFCGEK 311
Y	305 KFRNLVSFPRKHTTKRCKQCPVTPYRTVDGTSTNTPTGEQEVSTGL 354	Db	244 YFLFWAYNIVNLLSTQEFFGLNNCSGSNRDQAMCVTETLGMTHCCINPIYAFCGEK 303
Y	311 KFRRLSVFPRKHTTKRCKQCPVTPYRTVDGTSTNTPTGEQEVSTGL 360	Y	312 FRRYLSVFFRKHTTKRCKQCPVTPYRTVDGTSTNTPTGEQEVSTGL 360
Y	304 PRELIMINARY; PRT; 352 AA.	Db	304 PRELIMINARY; PRT; 352 AA.

RESULT 11		CRR5_CBRTO STANDARD; PRT; 352 AA.	
ID Q6WN96	PRELIMINARY;	PRT;	352 AA.
ID Q6WN96;			
AC			
DT 05-JUL-2004 (TREMBLrel. 27; Created)			
DT 05-JUL-2004 (TREMBLrel. 27; Last sequence update)			
DT 05-JUL-2004 (TREMBLrel. 27; Last annotation update)			
DB CC_chemokine receptor 5.			
GN Name=ccr5;			
OS Eukaryota; Metazoa; Chordata; Vertebrata; Sooty mangabey (Sooty mangabey) (Red-crowned mangabey) (Sooty mangabey).			
OC Mammalia; Butheria; Primates; Catarrhini; Eutheria; Eucoleostomi; Cercopitheciinae; Cercopithecidae;			
OC Leontocopithecus tamarinus (Gold-and-black lion tamarin); Piatyrrhini; Callitrichidae;			
OC Leontocopithecus			
OC NCBI_TaxID:58710;			
RN [1]			
SEQUENCE FROM N.A.			
RA Soares E.A.J.M., Schrargo C.G., Ribeiro I.P., Pissinatti A., Seunaez H.N., Russo C.A.M., Tanuri A., Soares M.A.; Submitted (APR 2003) to the EMBL/GenBank/DBJ databases.			
RL -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).			
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
DR EMBL:AY278747; AAQ00315.1; -.			
DR GO:GO:0016021; C:integral to membrane; IBA.			
DR GO:GO:0016493; F:C-C chemokine receptor activity; IBA.			
DR GO:GO:0004872; F:rhodopsin-like receptor activity; IBA.			
DR GO:GO:0015184; F:rhodopsin-like receptor activity; IBA.			
DR GO:GO:007186; P:G-protein coupled receptor protein signalin.			
DR InterPro: IPR000923; BlueCu_1.			
DR InterPro: IPR002240; CC_5_receptor.			
DR InterPro: IPR00355; Chmkine_receptor.			
DR InterPro: IPR000276; GPCR_RhoGDPsn.			
DR Pfam: PF00001; 7tm_1; 1.			
KW G-protein coupled receptor; Receptor; Transmembrane.			
PRINTS: PR00657; CCHBEMOKINER.			
PRINTS: PR01110; CHMOKINERS.			
DR PROSITE: PS00237; GPROPHODOPSIN.			
DR PROSITE: PS00196; COPPER_BLUE; UNKNOWN_1.			
DR PROSITE: PS000237; G_PROTEIN_RECIP_F1_1; 1.			
DR PROSITE: PS50062; G_PROTEIN_RECIP_F1_2; 1.			
KW G-protein coupled receptor; Receptor; Transmembrane.			
SEQUENCE 352 AA; 40458 MW; 0B4EA1B37CF16D90 CRC64;			
Query Match Score 72.5%; Score 1377; DB 2; Length 352;			
Best Local Similarity 75.2%; Fred. No. 3e-77; Indels 6; Gaps 2;			
Matches 258; Conservative 32; Mismatches 47;			
Qy 24 FDYDGA--PCKHFDYDQKIQGAGQLPLPLSYLVTFIFGVNMVLLINCKLKCLTDYL	81		
Ddb 10 YDIDGASEPRKIDVKQMGAHLLPLPLSYLVTFIFGVNMVLLINCKLKCLTDYL	69		
Qy 82 INLAISDLFLPITLPLWAHSANAEVFGNAMCKLFGLYHIGYFGGFLPILLTIDYLA	141		
Ddb 70 INLAISDLFLPITPWAHTYAZAGDNGFTGNTICQFLTGFLYFGEPSGFFILLTIDYLA	129		
Qy 142 IVAHFALKARTVTFCVVTSTIWLAVFASVPGIIIFTKCKEDSYVCGYFPRG---	197		
Ddb 130 IVAHFALKARTVTFCVVTSTIWLAVFASVPGIIIFTKCKEDSYVCGYFPRG---	189		
Qy 198 WNNFHFTIMRNIGLVLPLLMIVCYSGILKTLRCNEKEKHRAVRFITMIVYFLFWT	257		
Ddb 190 WKNFALKMVKYLGVLPLLMIVCYSGILKTLRCNEKEKHRAVRLIFTMIVYFLFWA	249		
Qy 258 PYNTVILLNTFQEFGFLNSCSTSOLDQATOVTETGMTHCCINPIIYAFGEKFRYLS	317		
Ddb 250 PYNTVILLNTYQEFGLNNCSNSRLDQMVTETGMTHCCVNPPIIYAFGEKFRYLV	309		
Qy 318 VFFRGIKTRKFCKQCPVFYRTVDGVTSTNTPSTGEOEVSAGL	360		
Ddb 310 VFFRKHAIAKCPERCFSIQRAPERANSVTSTGEOEVSAGL	352		
Qy 318 VFFRGIKTRKFCKQCPVFYRTVDGVTSTNTPSTGEOEVSAGL	360		
Ddb 310 VFFRKHAIAKCPERCFSIQRAPERANSVTSTGEOEVSAGL	352		

FT	VARIANT	107	L -> V	(in isolate 089).	
FT	VARIANT	134	V -> G	(in isolate 079).	
FT	VARIANT	146	V -> L	(in isolate 085 and isolate 089).	
FT	VARIANT	340	T -> I	(in isolate 079).	
SEQUENCE	SEQUENCE	352 AA;	40489 MW;	20A196B2A47E9CA CRC64;	
Query Match	Query Match	72.4%;	Score 1376;	DB 1; Length 352;	
Best Local Similarity	Best Local Similarity	76.4%;	Pred. No. 3-5e-77;		
Matches	Matches	262;	Conservative	31; Mismatches 44; Indels 6; Gaps 2;	
Qy	24 FDYD-Y-GAPCHKEPKDVKQIGAQOLLPLPYSVWTFGFVNMLVYLILINCKLKCLTDYL 81	Qy	24 FDYD-Y-GAPCHKEPKDVKQIGAQOLLPLPYSVWTFGFVNMLVYLILINCKLKCLTDYL 81	Qy	24 FDYD-Y-GAPCHKEPKDVKQIGAQOLLPLPYSVWTFGFVNMLVYLILINCKLKCLTDYL 81
Db	10 YDIDYTSEPKQKINQIAARLPLPYSVWTFGFVNMLVYLILINCKLKCLTDYL 69	Db	10 YDIDYTSEPKQKINQIAARLPLPYSVWTFGFVNMLVYLILINCKLKCLTDYL 69	Db	10 YDIDYTSEPKQKINQIAARLPLPYSVWTFGFVNMLVYLILINCKLKCLTDYL 69
Qy	82 INLAISDLFLITPLWAHSANNEWFGNAMCKLFGLHYIGFEGGIFPILLTIDRYLA 141	Qy	82 INLAISDLFLITPLWAHSANNEWFGNAMCKLFGLHYIGFEGGIFPILLTIDRYLA 141	Qy	82 INLAISDLFLITPLWAHSANNEWFGNAMCKLFGLHYIGFEGGIFPILLTIDRYLA 141
Db	70 INLAISDLFLITPLWAHSANNEWFGNAMCKLFGLHYIGFEGGIFPILLTIDRYLA 129	Db	70 INLAISDLFLITPLWAHSANNEWFGNAMCKLFGLHYIGFEGGIFPILLTIDRYLA 129	Db	70 INLAISDLFLITPLWAHSANNEWFGNAMCKLFGLHYIGFEGGIFPILLTIDRYLA 129
Qy	142 IVHAFALKARTVTFGVNTSITWLYAVFASVGPGLIFTKQREDSVYVCPYFP---RG 197	Qy	142 IVHAFALKARTVTFGVNTSITWLYAVFASVGPGLIFTKQREDSVYVCPYFP---RG 197	Qy	142 IVHAFALKARTVTFGVNTSITWLYAVFASVGPGLIFTKQREDSVYVCPYFP---RG 197
Db	130 IVHAFALKARTVTFGVNTSITWLYAVFASVGPGLIFTKQREGLYTCSPHPYSQYOF 189	Db	130 IVHAFALKARTVTFGVNTSITWLYAVFASVGPGLIFTKQREGLYTCSPHPYSQYOF 189	Db	130 IVHAFALKARTVTFGVNTSITWLYAVFASVGPGLIFTKQREGLYTCSPHPYSQYOF 189
Qy	198 WNNFHTIMRNLLGLVPLIMIVYCYSGILKTLLRCNEKKHRRAVTVFTIMIVYFLFWT 257	Qy	198 WNNFHTIMRNLLGLVPLIMIVYCYSGILKTLLRCNEKKHRRAVTVFTIMIVYFLFWT 257	Qy	198 WNNFHTIMRNLLGLVPLIMIVYCYSGILKTLLRCNEKKHRRAVTVFTIMIVYFLFWT 257
Db	190 WKNFQTLKIVTLGLVPLIMIVYCYSGILKTLLRCNEKKHRRAVTVFTIMIVYFLFWA 249	Db	190 WKNFQTLKIVTLGLVPLIMIVYCYSGILKTLLRCNEKKHRRAVTVFTIMIVYFLFWA 249	Db	190 WKNFQTLKIVTLGLVPLIMIVYCYSGILKTLLRCNEKKHRRAVTVFTIMIVYFLFWA 249
Qy	258 PYNIVLILNTFOBFFGLNSNCESTSQLDQATQVTEGLMTHCCINPIIYAFGEKFRRYLS 317	Qy	258 PYNIVLILNTFOBFFGLNSNCESTSQLDQATQVTEGLMTHCCINPIIYAFGEKFRRYLS 317	Qy	258 PYNIVLILNTFOBFFGLNSNCESTSQLDQATQVTEGLMTHCCINPIIYAFGEKFRRYLS 317
Db	250 PYNIVLILNTFOBFFGLNSNCSSSNRLDQAMQVTEGLMTHCCINPIIYAFGEKFRRYLL 309	Db	250 PYNIVLILNTFOBFFGLNSNCSSSNRLDQAMQVTEGLMTHCCINPIIYAFGEKFRRYLL 309	Db	250 PYNIVLILNTFOBFFGLNSNCSSSNRLDQAMQVTEGLMTHCCINPIIYAFGEKFRRYLL 309
Qy	318 VEFKRHKITKRFCKQCPVFYRTEVDGVTSTNTPSTGEVSAGL 360	Qy	318 VEFKRHKITKRFCKQCPVFYRTEVDGVTSTNTPSTGEVSAGL 360	Qy	318 VEFKRHKITKRFCKQCPVFYRTEVDGVTSTNTPSTGEVSAGL 360
Db	310 VFQKHAIRKRFCKCCSFQQEASERASSVTRSTGEQEVSGL 352	Db	310 VFQKHAIRKRFCKCCSFQQEASERASSVTRSTGEQEVSGL 352	Db	310 VFQKHAIRKRFCKCCSFQQEASERASSVTRSTGEQEVSGL 352
RESULT 14	RESULT 14	07776	PRELIMINARY;	PRT; 352 AA.	
ID	07776	ID	07776	PRELIMINARY;	
AC	AC	AC	07776;	PRT; 352 AA.	
DT	DT	DT	01-NOV-1998	(TREMBLrel. 08, Created)	
DT	DT	DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)	
DT	DT	DT	01-NAR-2004	(TREMBLrel. 26, Last annotation update)	
DE	DE	DE	DE	Chemokine receptor CCR5.	
GN	GN	GN	GN	Name=CCR5; Cercocebus torquatus torquatus.	
OS	OS	OS	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Cercopitheciidae; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercocebus.	
OC	OC	OC	OC	Cercopithecinae; Cercocebus.	
OC	OC	OC	OC	NCBI_TaxID=81944; NCBI_TaxID=81944;	
RN	RN	RN	RN	SEQUENCE FROM N.A.	
RP	RP	RP	RP	RP	
RX	RX	RX	RX	MEDLINE=91059829; PubMed=9841919; MEDLINE=91059829; PubMed=9841919; MEDLINE=91059829; PubMed=9841919;	
RA	RA	RA	RA	Chen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M.S., Lu C.Y., Aguilar R.F., Ho D.D., Marx P.A.;	
RA	RA	RA	RA	"Natural infection of a homozygous delta24 CCR5 red-capped mangabey with an R2b-tropic simian immunodeficiency virus.";	
RA	RA	RA	RA	J. Exp. Med. 188:2057-2059 (1998).	
RA	RA	RA	RA	- SUBCELLULAR LOCATION: Integral membrane protein (By similarity). ;	
RA	RA	RA	RA	- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. CC	
RA	RA	RA	RA	CC EMBL: AF084004; AAC24721; -.	
DR	DR	DR	DR	DR GO: GO:0016021; C:integral to membrane; IEA.	
DR	DR	DR	DR	DR GO: GO:0016493; P:C-C chemokine receptor activity; IEA.	
DR	DR	DR	DR	DR GO: GO:0004872; P:receptor activity; IEA.	
DR	DR	DR	DR	DR GO: GO:0001584; P:rhodopsin-like receptor activity; IEA.	
DR	DR	DR	DR	DR GO: GO:00007186; P:G-protein coupled receptor protein signalin. . ; IEA.	
DR	DR	DR	DR	DR InterPro: IPR02440; CC_5_Receptor.	
DR	DR	DR	DR	DR InterPro: IPR002240; GPCR_Rhodopsin.	
DR	DR	DR	DR	DR Prints: PF00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00237; CCACHEMOCKERINERS.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PS00237; GPROTEIN_RECEP_F1_1; 1.	
DR	DR	DR	DR	DR Prints: PS550262; G_PROTEIN_RECEP_F1_2; 1.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
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DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOKINERS.	
DR	DR	DR	DR	DR Prints: PR00237; GPCRHODOPSN.	
DR	DR	DR	DR	DR Prints: PR00001; 7tm_1; 1.	
DR	DR	DR	DR	DR Prints: PR00110; CHEMOK	

KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40475 MW; B3A63FDC4473D1D3 CRC64;

Query Match Score 1375; DB 2; Length 352;
 Best Local Similarity 76.1%; Pred. No. 4e-77;
 Matches 261; Conservative 32; Mismatches 44; Indels 6; Gaps 2;

Qy 24 FDYDY -GAPCHKFDVKQIGAQOLLPLPLSVPITFGPYGNMLVVLILINCKKLKCLTDIYL 81
 Db 10 YDIDYTTSEPCOKINVKQIAARLLPLPLSVPFGYGNMLVVLILINCKLKSMTDIYL 69

Qy 82 LNLAIISDLFLITLPLMAHSAANNEWFGNAMCKLFOLYHIGYGGTIPPLLTIDRYLA 141
 Db 70 LNLAIISDLFLITLPEWAHYAAQWDGNTMTCQLLGSLYPFGPSGTFPPLLTIDRYLA 129

Qy 142 IVHAVALALKARTVTFGVTVTIVLWAVAFASVPGIIFTKQKEDSYVCGYPFP---RG 197
 Db 130 IVHAVALALKARTVTFGVTVTIVLWAVAFASVPGIIFTKQKEDSYVCGYPFP---RG 197

Qy 198 WNNFHFTIMRNLLGLVPLIIMVYICSGILKTLLRCNEKGRHRAVVIFTIMIVYFLWT 257
 Db 190 WNNFHFTIKV1V1GLVPLIIMVYICSGILKTLLRCNEKGRHRAVVIFTIMIVYFLWA 249

Qy 258 PYNIVILLNTPOQFFGLSNCCESTSOLDOATQTYTETGMTHCCINPIIAYFGEKFRYLS 317
 Db 250 PYNIVILLNTPOQFFGLSNCCESTSOLDOATQTYTETGMTHCCINPIIAYFGEKFRYLS 309

Qy 318 VPFKRKHITKRFKQCPVYREFVTDGVTSTNGEVSAGL 360
 Db 310 VPFQKHLAKRFCCKCCSFQQEASERASSVTRSTGEDEISVGL 352

RESULT 15

Q8HZT9 PRELIMINARY; PRT; 352 AA.

AC Q8HZT9;
 DT 01-MAR-2003 (T-EMBL) [23, Created]
 DT 01-MAR-2003 (T-EMBL) [23, Last sequence update]
 DT 05-JUL-2004 (T-EMBL) [27, Last annotation update]
 DB Chemokine receptor CC5 (CC chemokine receptor 5).
 GN Name=ccr5;
 OS Saimiri sciureus (Common squirrel monkey).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 NCBI_TaxID=9521;

RN [1]

RP SEQUENCE FROM N.A.,
 RX MEDLINE=22174638; PubMed=12186836;
 RA LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
 RT "Blockade of HIV-1 infection of New World monkey cells occurs
 primarily at the stage of virus entry.";
 RL J. Exp. Med. 196:431-445 (2002).

RN [2]

RP SEQUENCE FROM N.A.,
 RX Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pisarinatti A.,
 RA Suanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

DR EMBL; AP42615; ANN14531_1; -.

DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
 DR InterPro; IPR002240; CC_5 receptor.
 DR InterPro; IPR000355; ChmKine receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO0657; CCHEMOKINER.
 DR PRINTS; PRO1110; CHEMOKINERS.

DR PRINTS; PRO0237; GPCRHHOOPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1; 1.
 DR PROSITE; PS50267; G PROTEIN RECEP_TF1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ 352 AA; 9FC896FB704647 CRC64;

Query Match Score 1375; DB 2; Length 352;
 Best Local Similarity 75.2%; Pred. No. 4e-77;
 Matches 258; Conservative 32; Mismatches 47; Indels 6; Gaps 2;

Qy 24 FDYDG -APCHKFDVKQIGQOLLPLPLSVPITFGVGNMLVVLILINCKLKLTDIYL 81
 Db 10 YDIDYGPSEPCRKIDTKQMGAQOLLPLISVPLFGVGNMLVVLILINCKLKSMTDIYL 69

Qy 82 INLAISDLFLITLPLWAHSANNEWFGNAMCKLFOLYHIGYGGTIPPLLTIDRYLA 141
 Db 70 INLAISDLFLITLPLWAHSANNEWFGNAMCKLFOLYHIGYGGTIPPLLTIDRYLA 129

Qy 142 IVHAVALKARTVTFGVTVTIVLWAVAFASVPGIIFTKQKEDSYVCGYPFP---RG 197
 Db 130 IVHAVALKARTVTFGVTVTIVLWAVAFASVPGIIFTKQKEDSYVCGYPFP---RG 197

Qy 142 IVHAVALKARTVTFGVTVTIVLWAVAFASVPGIIFTKQKEDSYVCGYPFP---RG 197
 Db 70 INLAISDLFLITLPLWAHSANNEWFGNAMCKLFOLYHIGYGGTIPPLLTIDRYLA 129

Qy 142 IVHAVALKARTVTFGVTVTIVLWAVAFASVPGIIFTKQKEDSYVCGYPFP---RG 197
 Db 130 IVHAVALKARTVTFGVTVTIVLWAVAFASVPGIIFTKQKEDSYVCGYPFP---RG 197

Qy 198 WNNFHFTIMRNLLGLVPLIIMVYICSGILKTLLRCNEKGRHRAVVIFTIMIVYFLWT 257
 Db 190 WNNFHFTIKV1V1GLVPLIIMVYICSGILKTLLRCNEKGRHRAVVIFTIMIVYFLWA 249

Qy 198 WNNFHFTIMRNLLGLVPLIIMVYICSGILKTLLRCNEKGRHRAVVIFTIMIVYFLWT 257
 Db 190 WNNFHFTIKV1V1GLVPLIIMVYICSGILKTLLRCNEKGRHRAVVIFTIMIVYFLWA 249

Qy 258 PYNIVILLNTPOQFFGLSNCCESTSOLDOATQTYTETGMTHCCINPIIAYFGEKFRYLS 317
 Db 250 PYNIVILLNTPOQFFGLSNCCESTSOLDOATQTYTETGMTHCCINPIIAYFGEKFRYLS 309

Qy 258 PYNIVILLNTPOQFFGLSNCCESTSOLDOATQTYTETGMTHCCINPIIAYFGEKFRYLS 317
 Db 250 PYNIVILLNTPOQFFGLSNCCESTSOLDOATQTYTETGMTHCCINPIIAYFGEKFRYLS 309

Qy 318 VPFKRKHITKRFKQCPVYREFVTDGVTSTNGEVSAGL 360
 Db 310 VPFQKHLAKRFCCKCCSFQQEASERASSVTRSTGEDEISVGL 352

Qy 318 VPFKRKHITKRFKQCPVYREFVTDGVTSTNGEVSAGL 360
 Db 310 VPFQKHLAKRFCCKCCSFQQEASERASSVTRSTGEDEISVGL 352

Search completed: June 9, 2005, 16:48:08
 Job time : 113.835 secs

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OM protein - protein search, using SW model

Run on: June 9, 2005, 16:37:43 ; Search time 29.9183 Seconds

(without alignments)
898.236 Million cell updates/sec

Title: US-10-791-166-4

Perfect score: 1900

Sequence: 1 MLSTSRSRPIRNTNESGEEV.....DGVTSTNTPSTGEQEVASGL 360

Scoring table: BL0SUMM2

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the result being printed.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1900	100.0	360	1 US-08-450-393A-4	Sequence 4, Appli
2	1900	100.0	360	3 US-08-446-69-4	Sequence 4, Appli
3	1900	100.0	360	3 US-09-045-583-50	Sequence 50, Appli
4	1900	100.0	360	4 US-09-534-185-50	Sequence 50, Appli
5	1900	100.0	360	4 US-09-131-827A-2	Sequence 2, Appli
6	1900	100.0	360	4 US-09-625-73-4	Sequence 4, Appli
7	1900	100.0	360	5 PCT-US95-00476-4	Sequence 4, Appli
8	1900	100.0	377	4 US-09-949-016-11221	Sequence 11221, A
9	1999.9	360	4 US-09-131-827A-20	Sequence 20, Appli	
10	1894	99.7	360	4 US-09-826-509-473	Sequence 473, Appli
11	1873	98.6	360	4 US-08-833-752-7	Sequence 7, Appli
12	1873	98.6	360	4 US-09-938-19-7	Sequence 7, Appli
13	1873	98.6	360	4 US-09-939-226B-7	Sequence 7, Appli
14	1849	97.3	360	3 US-09-045-583-51	Sequence 51, Appli
15	1849	97.3	360	4 US-09-534-185-51	Sequence 51, Appli
16	1838	96.7	347	1 US-08-461-244-3	Sequence 3, Appli
17	1651.5	86.9	374	1 US-08-450-393A-2	Sequence 2, Appli
18	1651.5	86.9	374	3 US-08-446-69-2	Sequence 14, Appli
19	1651.5	86.9	374	4 US-10-039-5693-14	Sequence 2, Appli
20	1651.5	86.9	374	4 US-09-625-573-2	Sequence 2, Appli
21	1651.5	86.9	374	5 PCT-US95-00476-2	Sequence 11222, A
22	1651.5	86.9	387	4 US-09-949-016-11222	Sequence 9, Appli
23	1568.5	82.6	344	3 US-08-466-343D-9	Sequence 9, Appli
24	1568.5	82.6	344	4 US-09-502-784A-9	Sequence 9, Appli
25	1473	77.5	329	4 US-09-502-783A-9	Sequence 9, Appli
26	1473	77.5	329	4 US-09-339-912A-9	Sequence 9, Appli
27	1473	77.5	329	4 US-09-195-662A-9	Sequence 9, Appli

RESULT 1

US-08-450-393A-4

; Sequence 4, Application US/08450393A

; Patent No. 5707815

; GENERAL INFORMATION:

; APPLICANT: Charco, Israel

; ADDRESS: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/450,393A

; FILING DATE: May 25, 1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Cbeir, Luann

; REGISTRATION NUMBER: 31,822

; REFERENCE/DOCKET NUMBER: UCAL-237/02US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-843-5165

; TELEFAX: 415-8857-0663

; TELEX: 380816coolevpa

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-450-393A-4

; Query Match

; Best Local Similarity 100.0%; Pred. No. 8.6e-151;

; Matches 360; Conservative 0; Mismatches 0; Gaps 0;

; Qy 1 MULTISRSRPIRNTNESSEEVTFDYGYAPCHKFDVKIGQLPPOLYSLYVIFGVGN 60

; Db 1 MULTISRSRPIRNTNESSEEVTFDYGYAPCHKFDVKIGQLPPOLYSLYVIFGVGN 60

RESULT 2
US-08-446-669-4
; Sequence 4, Application US/0844669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; ADDRESS: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nealey, Richard
; REGISTRATION NUMBER: 30,092
; TELECOMMUNICATION INFORMATION:
; TELEFAX: 415-843-5000
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-669-4

Query Match 100.0%; Score 1900; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.6e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSPRINTNESGEVTTFDYDGA^CKFDYKQIGAQOLLPLYSVLYFGVGN 60
Db 1 MLSTSRSPRINTNESGEVTTFDYDGA^CKFDYKQIGAQOLLPLYSVLYFGVGN 60
Qy 61 MLVVLILINCKLKLTDIYLNLAIISDLFLITLPLWAHSAAANEWVFGNAMCKLFTGly 120
Db 61 MLVVLILINCKLKLTDIYLNLAIISDLFLITLPLWAHSAAANEWVFGNAMCKLFTGly 120

RESULT 3
US-09-045-583-50
; Sequence 50, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOSS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MN1-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)42-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-045-583-50

Query Match 100.0%; Score 1900; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.6e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSPRINTNESGEVTTFDYDGA^CKFDYKQIGAQOLLPLYSVLYFGVGN 60
Db 1 MLSTSRSPRINTNESGEVTTFDYDGA^CKFDYKQIGAQOLLPLYSVLYFGVGN 60
Qy 61 MLVVLILINCKLKLTDIYLNLAIISDLFLITLPLWAHSAAANEWVFGNAMCKLFTGly 120
Db 61 MLVVLILINCKLKLTDIYLNLAIISDLFLITLPLWAHSAAANEWVFGNAMCKLFTGly 120

RESULT 4
US-09-534-185-50
 ; Sequence 50 Application US/09534185
 ; Patent No. 6403767
 ; GENERAL INFORMATION:
 ; APPLICANT: Graham, Gerard J. et al.
 ; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
 ; Receptor Superfamily and Uses
 ; Therefor
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; CURRENT APPLICATION DATA: Patent Release #1.0, Version #1.25
 ; APPLICATION NUMBER: US/09/534,185
 ; FILING DATE: 24-Mar-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragoras, Amy B.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: MN1-044
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 227-7400
 ; TELEFAX: (617) 742-4214
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 360 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Peptide
 ; FRAGMENT TYPE: internal
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
 ; US-09-534-185-50

Query Match 100.0%; Score 1900; DB 4; Length 360;
 Best Local Similarity 100.0%; Pred. No. 8.6e-151; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLVVLILINCKKLCKLTDIYLNLAISDLFLITPLWAHSAANEWVGNAMCKLFGLY 120

Qy 121 HIGYFGGIPFILLTIDRYLAIIVAVFALKARTTFFGVNTSVITMLAVAPASVPGIIFTK 180

Db 121 HIGYFGGIPFILLTIDRYLAIIVAVFALKARTTFFGVNTSVITMLAVAPASVPGIIFTK 180

Qy 181 CQKEDSVVYCGPYFRGMNFTIQRNLGVLPPLIMVTCYSGILKTLLRCRNEKRR 240

Db 181 CQKEDSVVYCGPYFRGMNFTIQRNLGVLPPLIMVTCYSGILKTLLRCRNEKRR 240

Qy 241 AVRIFTIMIVYFLWTPNIVLINTFQEFFGSNCESTSOLQDQATQVETLGHTHCC 300

Db 241 AVRIFTIMIVYFLWTPNIVLINTFQEFFGSNCESTSOLQDQATQVETLGHTHCC 300

Qy 301 NPIIYAFVGKFRRLSVFPRKHITKRFCKOCQCPYTFETDGVTSNTPTGEQEVSA 360

Db 301 NPIIYAFVGKFRRLSVFPRKHITKRFCKOCQCPYTFETDGVTSNTPTGEQEVSA 360

Db 301 NPIIYAFVGKFRRLSVFPRKHITKRFCKOCQCPYTFETDGVTSNTPTGEQEVSA 360

RESULT 5
US-09-131-827A-2
 ; Sequence 2, Application US/09131827A
 ; Patent No. 6600030
 ; GENERAL INFORMATION:
 ; APPLICANT: Dean, Michael
 ; APPLICANT: O'Brien, Stephen J.
 ; APPLICANT: Smith, Michael
 ; APPLICANT: Carrington, Mary
 ; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
 ; FILE REFERENCE: 14014-0333
 ; CURRENT APPLICATION NUMBER: US/09/131,827A
 ; CURRENT FILING DATE: 1998-08-10
 ; PRIOR APPLICATION NUMBER: 60/055,659
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 360
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-131-827A-2

Query Match 100.0%; Score 1900; DB 4; Length 360;
 Best Local Similarity 100.0%; Pred. No. 8.6e-151; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFRNTNESGEVTTFFDYYGAPCHKFVDKQIGAQQLPPLYSVFIGFVG 60

Db 1 MLSTSRSRFRNTNESGEVTTFFDYYGAPCHKFVDKQIGAQQLPPLYSVFIGFVG 60

Qy 61 MLVVLILINCKKLCKLTDIYLNLAISDLFLITPLWAHSAANEWVGNAMCKLFGLY 120

Db 61 MLVVLILINCKKLCKLTDIYLNLAISDLFLITPLWAHSAANEWVGNAMCKLFGLY 120

Qy 121 HIGYFGGIPFILLTIDRYLAIIVAVFALKARTTFFGVNTSVITMLAVAPASVPGIIFTK 180

Db 121 HIGYFGGIPFILLTIDRYLAIIVAVFALKARTTFFGVNTSVITMLAVAPASVPGIIFTK 180

Qy 181 CQKEDSVVYCGPYFRGMNFTIQRNLGVLPPLIMVTCYSGILKTLLRCRNEKRR 240

Db 181 CQKEDSVVYCGPYFRGMNFTIQRNLGVLPPLIMVTCYSGILKTLLRCRNEKRR 240

Qy 301 NPIIYAFVGKFRRLSVFPRKHITKRFCKOCQCPYTFETDGVTSNTPTGEQEVSA 360

Db 301 NPIIYAFVGKFRRLSVFPRKHITKRFCKOCQCPYTFETDGVTSNTPTGEQEVSA 360

Qy 61 MLVVLILINCKKLCKLTDIYLNLAISDLFLITPLWAHSAANEWVGNAMCKLFGLY 120

RESULT 6
US-09-625-573-4

Sequence 4, Application US/09625573
 Patent No. 6730301
 GENERAL INFORMATION:
 APPLICANT: Chario, Israel
 Coughlin, Shaun
 TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT PROTEIN RECEPTORS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooley Godward Castro Huddleston & Tatum
 STREET: 5 Palo Alto Square
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94306-2155
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/625,573
 FILING DATE: 25-Jul-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/446,669
 FILING DATE: May 25, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Neely, Richard
 REGISTRATION NUMBER: 30,092
 TELEPHONE: 415-843-5000
 TELEFAX: 415-857-0663
 TELEX: 380816cooleypa
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 360 amino acids
 TOPOLogy: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-625-573-4

Query Match 100.0%; Score 1900; DB 4; Length 360;
 Best Local Similarity 100.0%; Pred. No. 8..6e-151;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRTRNTNESEGVTTFFDYDGA^PCKFDVQIGAQOLLPP^SLVL^VF^GVGN 60
 Db 1 MLVLLILINCKLKCLTDYLNLNAISDLFLITLPLWAHSAANEWVGNA^CKLF^GLY 120
 Qy 61 MLVLLILINCKLKCLTDYLNLNAISDLFLITLPLWAHSAANEWVGNA^CKLF^GLY 120
 Db 61 MLVLLILINCKLKCLTDYLNLNAISDLFLITLPLWAHSAANEWVGNA^CKLF^GLY 120
 Qy 121 HIGYFGG^IFFI^LITL^TD^RYLA^VH^AV^AP^LK^AT^TV^FG^VT^ST^TW^LA^VF^AS^VP^GI^FTK 180
 Db 121 HIGYFGG^IFFI^LITL^TD^RYLA^VH^AV^AP^LK^AT^TV^FG^VT^ST^TW^LA^VF^AS^VP^GI^FTK 180

Qy 121 HIGYFGG^IFFI^LITL^TD^RYLA^VH^AV^AP^LK^AT^TV^FG^VT^ST^TW^LA^VF^AS^VP^GI^FTK 180
 Db 121 HIGYFGG^IFFI^LITL^TD^RYLA^VH^AV^AP^LK^AT^TV^FG^VT^ST^TW^LA^VF^AS^VP^GI^FTK 180

Qy 181 CQEDSVYVC^GP^FPRGNNNFTIMRNFLGVL^VPL^LIMIVC^SGIL^TLRCNEKGRHR 240
 Db 181 CQEDSVYVC^GP^FPRGNNNFTIMRNFLGVL^VPL^LIMIVC^SGIL^TLRCNEKGRHR 240
 Qy 241 AYVIFTIMIVYPLFWTPNIVILLNTQEFGLSNCESTSOLDQATQVETIGMTHCC1 300
 Db 241 AYVIFTIMIVYPLFWTPNIVILLNTQEFGLSNCESTSOLDQATQVETIGMTHCC1 300
 Qy 301 NPIIYAFGEKFRRLSVFRRKHTIKRKFCQCPVFYRETVDGVTSTNTPSTGEQEVASGL 360
 Db 301 NPIIYAFGEKFRRLSVFRRKHTIKRKFCQCPVFYRETVDGVTSTNTPSTGEQEVASGL 360

RESULT 7
PCT-US95-00476-4
 Sequence 4, Application PC/TU9500476
 GENERAL INFORMATION:
 APPLICANT: The Regents of the University of California
 TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Robbins, Berliner & Carson
 STREET: 201 N. Figueroa Street, 5th Floor
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90012-2628
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/00476
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Berliner, Robert
 REGISTRATION NUMBER: 20,121
 REFERENCE DOCKET NUMBER: 5555-291
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-977-1001
 TELEFAX: 310-977-1003
 TELEX:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 360 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-00476-4

Query Match 100.0%; Score 1900; DB 5; Length 360;
 Best Local Similarity 100.0%; Pred. No. 8..6e-151;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRTRNTNESEGVTTFFDYDGA^PCKFDVQIGAQOLLPP^SLVL^VF^GVGN 60
 Db 1 MLSTSRSRTRNTNESEGVTTFFDYDGA^PCKFDVQIGAQOLLPP^SLVL^VF^GVGN 60
 Qy 61 MLVLLILINCKLKCLTDYLNLNAISDLFLITLPLWAHSAANEWVGNA^CKLF^GLY 120
 Db 61 MLVLLILINCKLKCLTDYLNLNAISDLFLITLPLWAHSAANEWVGNA^CKLF^GLY 120
 Qy 121 HIGYFGG^IFFI^LITL^TD^RYLA^VH^AV^AP^LK^AT^TV^FG^VT^ST^TW^LA^VF^AS^VP^GI^FTK 180
 Db 121 HIGYFGG^IFFI^LITL^TD^RYLA^VH^AV^AP^LK^AT^TV^FG^VT^ST^TW^LA^VF^AS^VP^GI^FTK 180

Qy 181 CQEDSVYVC^GP^FPRGNNNFTIMRNFLGVL^VPL^LIMIVC^SGIL^TLRCNEKGRHR 240
 Db 181 CQEDSVYVC^GP^FPRGNNNFTIMRNFLGVL^VPL^LIMIVC^SGIL^TLRCNEKGRHR 240
 Qy 241 AYVIFTIMIVYPLFWTPNIVILLNTQEFGLSNCESTSOLDQATQVETIGMTHCC1 300
 Db 241 AYVIFTIMIVYPLFWTPNIVILLNTQEFGLSNCESTSOLDQATQVETIGMTHCC1 300
 Qy 301 NPIIYAFGEKFRRLSVFRRKHTIKRKFCQCPVFYRETVDGVTSTNTPSTGEQEVASGL 360
 Db 301 NPIIYAFGEKFRRLSVFRRKHTIKRKFCQCPVFYRETVDGVTSTNTPSTGEQEVASGL 360

RESULT 8
US-09-949-016-11221

Sequence 11221, Application US/0949016
; Patent No. 6812319 ; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE INVENTION: CL001307 FILE REFERENCE: CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT PILING DATE: 2000-04-14 PRIOR PILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-11-11
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR PILING DATE: 2000-09-08
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11221 LENGTH: 377
; TYPE: PRT ORGANISM: Human US-09-949-016-11221

Query Match 100.0%; Score 1900; DB 4; Length 377; Best Local Similarity 99.7%; Pred. No. 1e-150; Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ML-STSRSRFRNTNESGERVTTFDYDGAPECHKFDVKGQLPLPLSVLFIGFVGNN 60
Db 1 ML-STSRSRFRNTNESGERVTTFDYDGAPECHKFDVKGQLPLPLSVLFIGFVGNN 60

Qy 61 MLVVLILINCKKLKCLTDIYLNLAISDLFLITPLWAHSAANEWVFGNAMCKLFTGGLY 120
Db 61 MLVVLILINCKKLKCLTDIYLNLAISDLFLITPLWAHSAANEWVFGNAMCKLFTGGLY 120

Qy 121 HIGHFGIFFLILLTIDRYIAIVHAFALKARTTGFVVTSTVTLVAVFASVGIIFTK 180
Db 121 HIGHFGIFFLILLTIDRYIAIVHAFALKARTTGFVVTSTVTLVAVFASVGIIFTK 180

Qy 181 CQEDSVVYCGPYPRGMNNFHITMRLNLGLVPLIMVTCYSGILKTLLRCNEKKHR 240
Db 181 CQEDSVVYCGPYPRGMNNFHITMRLNLGLVPLIMVTCYSGILKTLLRCNEKKHR 240

Qy 241 AVRVIPTIMIVYELFWTPNIVILANTFOBFFGLSNCESTSOLQATOVTETLGTMTHCC 300
Db 241 AVRVIPTIMIVYELFWTPNIVILANTFOBFFGLSNCESTSOLQATOVTETLGTMTHCC 300

Qy 301 NPIIYAFGEKFRYLISVFRKHITRKFCQCPVYRETVDGTISTNTSTGEQEVASGL 360
Db 301 NPIIYAFGEKFRYLISVFRKHITRKFCQCPVYRETVDGTISTNTSTGEQEVASGL 360

RESULT 10 US-09-826-509-473
; Sequence 473, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-01-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 473
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens US-09-826-509-473

Query Match 99.7%; Score 1894; DB 4; Length 360; Best Local Similarity 99.7%; Pred. No. 2.7e-150; Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ML-STSRSRFRNTNESGERVTTFDYDGAPECHKFDVKGQLPLPLSVLFIGFVGNN 60
Db 1 MLVVLILINCKKLKCLTDIYLNLAISDLFLITPLWAHSAANEWVFGNAMCKLFTGGLY 120
Qy 61 MLVVLILINCKKLKCLTDIYLNLAISDLFLITPLWAHSAANEWVFGNAMCKLFTGGLY 120
Db 121 HIGHFGIFFLILLTIDRYIAIVHAFALKARTTGFVVTSTVTLVAVFASVGIIFTK 180
Db 121 HIGHFGIFFLILLTIDRYIAIVHAFALKARTTGFVVTSTVTLVAVFASVGIIFTK 180

Query Match 98.6%; Score 1873; DB 4; Length 360;
 Best Local Similarity 98.3%; Pred. No. 1..5e-14;
 Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFRNTNESGEVTTFFDYGAPCKFDYKQIGQLLPPPLSIVFIFGVGN 60
 Db 1 MLSTSRSRFRNTNESGEVTTFFDYGAPCKFDYKQIGQLLPPPLSIVFIFGVGN 60
 Qy 61 MLVLILINCKKLKCLTDIYLNLIAISDLFLITLPLWAHSAANEWFGNAMCKLFGLY 120
 Db 61 MLVLILINCKKLKCLTDIYLNLIAISDLFLITLPLWAHSAANEWFGNAMCKLFGLY 120
 Qy 121 HIGYFGGIFFTILLTIDRYLAIVHAFALKARTVTEGVTVSITMLVAEVASVPGIFTK 180
 Db 121 HIGYFGGIFFTILLTIDRYLAIVHAFALKARTVTEGVTVSITMLVAEVASVPGIFTK 180
 Qy 181 COKEDSVYVCGPYPRGMNNFTIMRNLLGILVPLLINVTCYSGILKTLRCRNEKCHR 240
 Db 181 COKEDSVYVCGPYPRGMNNFTIMRNLLGILVPLLINVTCYSGILKTLRCRNEKCHR 240

RESULT 11
 US-08-833-752-7
 ; Sequence 7, Application US/088333752
 ; GENERAL INFORMATION:
 ; Patent No. 6448375
 ; GENERAL INFORMATION:
 ; APPLICANT: SAMSON, MICHEL
 ; APPLICANT: PARMENTIER, MARC
 ; APPLICANT: VASSART, GILBERT
 ; APPLICANT: LIBERT, FREDERICK
 ; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
 ; NUMBER OF SEQUENCES: 17
 ; ADDRESS: Knobbe, Martens, Olson & Bear
 ; STREET: 620 Newport Center Drive 16th Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/833,752
 ; FILING DATE: 9-APR-1997
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Altman, Daniel E
 ; REGISTRATION NUMBER: 34,115
 ; REFERENCE DOCKET NUMBER:
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 360 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 6448375e
 ; US-08-833-752-7

Query Match 98.6%; Score 1873; DB 4; Length 360;
 Best Local Similarity 98.3%; Pred. No. 1..5e-14;
 Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFRNTNESGEVTTFFDYGAPCKFDYKQIGQLLPPPLSIVFIFGVGN 60
 Db 1 MLSTSRSRFRNTNESGEVTTFFDYGAPCKFDYKQIGQLLPPPLSIVFIFGVGN 60
 Qy 61 MLVLILINCKKLKCLTDIYLNLIAISDLFLITLPLWAHSAANEWFGNAMCKLFGLY 120
 Db 61 MLVLILINCKKLKCLTDIYLNLIAISDLFLITLPLWAHSAANEWFGNAMCKLFGLY 120
 Qy 121 HIGYFGGIFFTILLTIDRYLAIVHAFALKARTVTEGVTVSITMLVAEVASVPGIFTK 180
 Db 121 HIGYFGGIFFTILLTIDRYLAIVHAFALKARTVTEGVTVSITMLVAEVASVPGIFTK 180
 Qy 181 COKEDSVYVCGPYPRGMNNFTIMRNLLGILVPLLINVTCYSGILKTLRCRNEKCHR 240
 Db 181 COKEDSVYVCGPYPRGMNNFTIMRNLLGILVPLLINVTCYSGILKTLRCRNEKCHR 240

Query Match 98.6%; Score 1873; DB 4; Length 360;
 Best Local Similarity 98.3%; Pred. No. 1.5e-148;
 Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLSTSRSRTRNTNESGEVTTFDDYDGA^PCKFDVKOIGAQOLLPLPLS^LYF^IGF^VGN 60
 Db 1 MLVSLLINCKLKCLTDIYLNLAIASDLFLITLPLMAHSAANNEWFGNAMCKLF^GLY 120

Qy 61 MLVSLLINCKLKCLTDIYLNLAIASDLFLITLPLMAHSAANNEWFGNAMCKLF^GLY 120
 Db 61 MLVSLLINCKLKCLTDIYLNLAIASDLFLITLPLMAHSAANNEWFGNAMCKLF^GLY 120

Qy 121 HIGYGGI^PILLTIDRYLAIVHAVALKARTT^TMRN^TLGVLPLLI^NVI^CYSGIL^KLTCRNEKGRHR 240
 Db 121 HIGYGGI^PILLTIDRYLAIVHAVALKARTT^TMRN^TLGVLPLLI^NVI^CYSGIL^KLTCRNEKGRHR 240

Qy 181 COKEDSVVYCGYP^PRGMNNFHTMRLN^TLGVLPLLI^NVI^CYSGIL^KLTCRNEKGRHR 240
 Db 181 COKEDSVVYCGYP^PRGMNNFHTMRLN^TLGVLPLLI^NVI^CYSGIL^KLTCRNEKGRHR 240

Qy 61 COKEDSVVYCGYP^PRGMNNFHTMRLN^TLGVLPLLI^NVI^CYSGIL^KLTCRNEKGRHR 240
 Db 61 COKEDSVVYCGYP^PRGMNNFHTMRLN^TLGVLPLLI^NVI^CYSGIL^KLTCRNEKGRHR 240

Qy 181 COKEDSVVYCGYP^PRGMNNFHTMRLN^TLGVLPLLI^NVI^CYSGIL^KLTCRNEKGRHR 240
 Db 181 COKEDSVVYCGYP^PRGMNNFHTMRLN^TLGVLPLLI^NVI^CYSGIL^KLTCRNEKGRHR 240

Qy 241 AYRVLIFTIMVYFLFWTPNIVLNLNTFOFFGLSNCEST^SQDQATOVTETLGMTHCC^I 300
 Db 241 AYRVLIFTIMVYFLFWTPNIVLNLNTFOFFGLSNCEST^SQDQATOVTETLGMTHCC^I 300

Qy 301 NPIIYAFVCEBKFRYL^SVERKHLTKRFCKQCPV^FYRETVDGT^TSTNP^STGPQEVSAGL 360
 Db 301 NPIIYAFVCEBKFRYL^SVERKHLTKRFCKQCPV^FYRETVDGT^TSTNP^STGPQEVSAGL 360

RESULT 14
 US-09-045-583-51
 ; Sequence 51, Application US/09045583
 ; Patent No. 6287805
 ; GENERAL INFORMATION:
 ; APPLICANT: Granham, Gerard J. et al.
 ; TITLE OF INVENTION: No. 6287805-1 Molecules of the G Protein-Coupled
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAJIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/045,583
 ; FILING DATE: 20-MAR-98
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragoras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: MN1-044
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-1214
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 360 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 US-09-045-583-51

Query Match 97.3%; Score 1849; DB 3; Length 360;
 Best Local Similarity 97.2%; Pred. No. 1.5e-146;
 Matches 350; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRTRNTNESGEVTTFDDYDGA^PCKFDVKOIGAQOLLPLPLS^LYF^IGF^VGN 60
 Db 1 MLSTSRSRTRNTNESGEVTTFDDYDGA^PCKFDVKOIGAQOLLPLPLS^LYF^IGF^VGN 60

Qy 61 MLVVLINCKLKCLTDIYLNLAIASDLFLITLPLMAHSAANNEWFGNAMCKLF^GLY 120
 Db 61 MLVVLINCKLKCLTDIYLNLAIASDLFLITLPLMAHSAANNEWFGNAMCKLF^GLY 120

Qy 121 HIGYGGI^PILLTIDRYLAIVHAVALKARTT^TMRN^TLGVLPLLI^NVI^CYSGIL^KLTCRNEKGRHR 240
 Db 121 HIGYGGI^PILLTIDRYLAIVHAVALKARTT^TMRN^TLGVLPLLI^NVI^CYSGIL^KLTCRNEKGRHR 240

Qy 181 COKEDSVVYCGYP^PRGMNNFHTMRLN^TLGVLPLLI^NVI^CYSGIL^KLTCRNEKGRHR 240
 Db 181 COKEDSVVYCGYP^PRGMNNFHTMRLN^TLGVLPLLI^NVI^CYSGIL^KLTCRNEKGRHR 240

Qy 241 AYRVLIFTIMVYFLFWTPNIVLNLNTFOFFGLSNCEST^SQDQATOVTETLGMTHCC^I 300
 Db 241 AYRVLIFTIMVYFLFWTPNIVLNLNTFOFFGLSNCEST^SQDQATOVTETLGMTHCC^I 300

Qy 301 NPIIYAFVCEBKFRYL^SVERKHLTKRFCKQCPV^FYRETVDGT^TSTNP^STGPQEVSAGL 360
 Db 301 NPIIYAFVCEBKFRYL^SVERKHLTKRFCKQCPV^FYRETVDGT^TSTNP^STGPQEVSAGL 360

US-09-534-185-51
 ; Sequence 51 Application US/09534185
 ; Patent No 6403767

GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.
 TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
 Heptahelical Receptor Superfamily and Uses
 Therefor

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185

FILING DATE: 24-Mar-2000

CLASSIFICATION: <Unknown>

PRIORITY DATA:

APPLICATION NUMBER: 09/045,583

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNI-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 360 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 51:

US-09-534-185-51

Query Match 97.3%; Score 1849; DB 4; Length 360;
 Best Local Similarity 97.2%; Pred. No. 1..5e-146;
 Matches 350; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MLSTSRSPRINTNESGEVTTPEPDYDGAAPCKFDVKQIGQLLPLPLSFLVIFGVGN 60

Db 1 MLSTSRSPRINTNGSGEVTTPEPDYDGAAPCKFDVKQIGQLLPLPLSFLVIFGVGN 60

Qy 61 MLVLILINCKKLCKLTDIYLINLAISDLFLITLPLWAHSAAANEWFGNAMCKLFTGLY 120

Db 61 MLVLILINCKKLCKLTDIYLINLAISDLFLITLPLWAHSAAANEWFGNAMCKLFTGLY 120

Qy 121 HIGYGGGFFIILITIDRYLAIVTHAVFKARTTTCGVTTVITWLVAVASVPGILIFTK 180

Db 121 HIGYGGGFFIILITIDRYLAIVTHAVFKARTTTCGVTTVITWLVAVASVPGILIFTK 180

Qy 181 CQEDSVYVCGPFPRGNNFPRGMNNFTIMRNLLGVPLLMVTCGILTLRCNEKGRHR 240

Db 181 CQEDSVYVCGPFPRGNNFTIMRNLLGVPLLMVTCGILTLRCNEKGRHR 240

Qy 241 AYRIFTIMIVYFLWTPYNTVILLNTFOEFGNSNCESTSOLDATOYTBTLGMTHCII 300

Db 241 AYRIFTIMIVYFLWTPYNTVILLNTFOEFGNSNCESTSQRDQATQVTLGTMHCII 300

Qy 301 NPIIYAFGEKFRYLSMFRKTYTKRCKQCPVYFRETVDGVTSTNTPSTGEQEVSAGL 360

Db 301 NPIIYAFGEKFRYLSMFRKTYTKRCKQCPVYFRETVDGVTSTNTPSTAEQEVSAGL 360

Result No.	Score	Query Match Length	DB ID	Description
1	1900	100.0	360 9 US-09-131-827A-2	Sequence 2, Appli
2	1900	100.0	360 14 US-10-225-567A-460	Sequence 460, App
3	1900	100.0	360 14 US-10-164-649-50	Sequence 50, Appli
4	1900	100.0	360 14 US-10-233-423-64	Sequence 64, Appli
5	1900	100.0	360 14 US-10-439-845-8	Sequence 8, Appli
6	1900	100.0	360 16 US-10-741-601-285	Sequence 285, App
7	1900	100.0	360 16 US-10-791-592-4	Sequence 4, Appli
8	1900	100.0	360 16 US-10-791-166-4	Sequence 4, Appli
9	1900	100.0	360 16 US-10-700-313-8	Sequence 8, Appli
10	1900	100.0	360 17 US-10-486-471-4	Sequence 4, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1900	100.0	360 9 US-09-131-827A-2	Sequence 2, Appli
2	1900	100.0	360 14 US-10-225-567A-460	Sequence 460, App
3	1900	100.0	360 14 US-10-164-649-50	Sequence 50, Appli
4	1900	100.0	360 14 US-10-233-423-64	Sequence 64, Appli
5	1900	100.0	360 14 US-10-439-845-8	Sequence 8, Appli
6	1900	100.0	360 16 US-10-741-601-285	Sequence 285, App
7	1900	100.0	360 16 US-10-791-592-4	Sequence 4, Appli
8	1900	100.0	360 16 US-10-791-166-4	Sequence 4, Appli
9	1900	100.0	360 16 US-10-700-313-8	Sequence 8, Appli
10	1900	100.0	360 17 US-10-486-471-4	Sequence 4, Appli

ALIGMENTS

RESULT 1	US-09-131-827A-2	;	Sequence 2, Application US/09131827A
		;	PARENT NO. US20020038469A1
		;	GENERAL INFORMATION:
		;	APPLICANT: Dean, Michael
		;	APPLICANT: O'Brien, Stephen J.
		;	APPLICANT: Smith, Michael
		;	APPLICANT: Carrington, Mary
		;	TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
		;	NUMBER OF SEQ ID NOS: 20
		;	FILE REFERENCE: 14014_0333
		;	CURRENT APPLICATION NUMBER: US/09-131-827A
		;	PRIOR APPLICATION NUMBER: 60/055, 659
		;	PRIOR FILING DATE: 1997-08-14
		;	SOFTWARE: FastSBQ for Windows Version 4.0
		;	SEQ ID NO 2
		;	TYPE: PRT
		;	ORGANISM: Homo sapiens
		;	US-09-131-827A-2

Query Match 100.0% Score 1900 DB 9; Length 360;

Best Local Similarity 100.0%; Pred. No. 4.5e-150; Mismatches 0; Indels 0; Gaps 0;

1 MLSTSRSRIRNTNESEGEVTFFDYGAPCKHFDYKQIGAQQLPPPLYSLVPFGVGN 60
 1 MLSTSRSRIRNTNESEGEVTFFDYGAPCKHFDYKQIGAQQLPPPLYSLVPFGVGN 60
 61 MLVVLINCKLKLCLTDIYLNLAISSDILFLITLPWAHSAANEWGNAMECKLFGLY 120

RESULT 2
US-10-225-567A-460

Sequence 460, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIgenic PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225, 567A
PRIORITY FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257, 144
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 460
LENGTH: 360
TYPE: PPT
ORGANISM: Homo sapiens

US-10-225-567A-460

Query Match 100.0%; Score 1900; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFRNTNESGBEVTFFDYGAPCKFDYKQIGQOLLPLPLSIVFPGVGN 60
Db 1 MLSTSRSRFRNTNESGBEVTFFDYGAPCKFDYKQIGQOLLPLPLSIVFPGVGN 60

Qy 61 MLVLILINCKLKCLTDYLNLNLASIDLFLITLPLWAHSAAANEWFGNAMCKLFTGLY 120
Db 61 MLVLILINCKLKCLTDYLNLNLASIDLFLITLPLWAHSAAANEWFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFFILITIDRYLAIVHAFALKARTVTCGVTVSITMLVAFAVSPGIFTK 180
Db 121 HIGYFGGIFFFILITIDRYLAIVHAFALKARTVTCGVTVSITMLVAFAVSPGIFTK 180

Qy 181 COKEDESYVCGPYPPRGNNFTIMRNLLGVLPLLMIVCYSGILKTLRNEKGRHR 240
Db 181 COKEDESYVCGPYPPRGNNFTIMRNLLGVLPLLMIVCYSGILKTLRNEKGRHR 240

Qy 241 AVRIFTIMIVYFLFWTNPYINVILLNTQEFFGNSCESTSSOLDATQVTELGGMTHCCI 300
Db 241 AVRIFTIMIVYFLFWTNPYINVILLNTQEFFGNSCESTSSOLDATQVTELGGMTHCCI 300

Qy 301 NPIIYAFGEKPFRRYLSVFFRKTKFCQCPVYRETVDGVTSITNTPSTGEOEVSAGL 360
Db 301 NPIIYAFGEKPFRRYLSVFFRKTKFCQCPVYRETVDGVTSITNTPSTGEOEVSAGL 360

; Sequence 50, Application US/10164649
; Publication No. US20030162943A1
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. US20030162943A1 Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/164, 649
FILING DATE: 07-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/045, 583
FILING DATE: 20-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mandersoures, Amy E.
REGISTRATION NUMBER: 36, 207
RECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)42-4214
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-164-649-50

Query Match 100.0%; Score 1900; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFRNTNESGBEVTFFDYGAPCKFDYKQIGQOLLPLPLSIVFPGVGN 60
Db 1 MLSTSRSRFRNTNESGBEVTFFDYGAPCKFDYKQIGQOLLPLPLSIVFPGVGN 60

Qy 61 MLVLILINCKLKCLTDYLNLNLASIDLFLITLPLWAHSAAANEWFGNAMCKLFTGLY 120
Db 61 MLVLILINCKLKCLTDYLNLNLASIDLFLITLPLWAHSAAANEWFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFFILITIDRYLAIVHAFALKARTVTCGVTVSITMLVAFAVSPGIFTK 180
Db 121 HIGYFGGIFFFILITIDRYLAIVHAFALKARTVTCGVTVSITMLVAFAVSPGIFTK 180

Qy 181 COKEDESYVCGPYPPRGNNFTIMRNLLGVLPLLMIVCYSGILKTLRNEKGRHR 240
Db 181 COKEDESYVCGPYPPRGNNFTIMRNLLGVLPLLMIVCYSGILKTLRNEKGRHR 240

Qy 241 AVRIFTIMIVYFLFWTNPYINVILLNTQEFFGNSCESTSSOLDATQVTELGGMTHCCI 300
Db 241 AVRIFTIMIVYFLFWTNPYINVILLNTQEFFGNSCESTSSOLDATQVTELGGMTHCCI 300

Qy 301 NPIIYAFGEKPFRRYLSVFFRKTKFCQCPVYRETVDGVTSITNTPSTGEOEVSAGL 360
Db 301 NPIIYAFGEKPFRRYLSVFFRKTKFCQCPVYRETVDGVTSITNTPSTGEOEVSAGL 360

Sequence 64, Application US/10239423
 Publication No. US20030186889A1
 GENERAL INFORMATION:
 ; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
 ; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
 ; Cell Surface Proteome of Tumor and Inflammation Cells and
 ; Diseases and Inflammatory Diseases,
 ; PREFERABLY WITH THE AID OF SPECIFIC CHEMOKINE RECEPTOR/LIGAND INTERACTION
 ; FILE REFERENCE: 022217US
 ; CURRENT APPLICATION NUMBER: US/10/239,423
 ; CURRENT FILING DATE: 2002-09-23
 ; PRIOR APPLICATION NUMBER: DE10016013.1
 ; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 64
 ; LENGTH: 360
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
 ; US-10-239-423-64

Query Match Score 1900; DB 14; Length 360;
 Best Local Similarity 100.0%; Pred. No. 4.5e-150;
 Matches 360; Conservative 0; Gaps 0;
 Qy 1 MLSTSRSPRINTNESGEVTTFDYDGAQCHKFDVQIGAQQLPLYSVLPFGVGQN 60
 Db 1 MLSTSRSPRINTNESGEVTTFDYDGAQCHKFDVQIGAQQLPLYSVLPFGVGQN 60
 Qy 61 MLYVLLINCKLKCLDIYLNIAISDLFLITLPLWAHSAAANEWVGNAMCKLFGLY 120
 Db 61 MLYVLLINCKLKCLDIYLNIAISDLFLITLPLWAHSAAANEWVGNAMCKLFGLY 120
 Qy 121 HIGYFGGIPPIILITIDRYLAIVHAPALKARTTIEGVTSVITWLAVFASVPGIIFTK 180
 Db 121 HIGYFGGIPPIILITIDRYLAIVHAPALKARTTIFGVVTSVITWLAVFASVPGIIFTK 180
 Qy 181 CQEDSVTVCGPYPGRNNNFTIMRNLTGVLPLINIVTCYGLKLTKLRCNEKGRHR 240
 Db 181 CQEDSVTVCGPYPGRNNNFTIMRNLTGVLPLINIVTCYGLKLTKLRCNEKGRHR 240
 Qy 241 AYRVFTIMIVYLFWTPNIVILLNTQFFGLSNCESTSOLDQATOVTETLGMTHCCI 300
 Db 241 AYRVFTIMIVYLFWTPNIVILLNTQFFGLSNCESTSOLDQATOVTETLGMTHCCI 300
 Qy 301 NPIIYAFGEKFRRLSVPRPKITKRPCKQCPVYFYRTDVGTSTNPSTGEQVSAGL 360
 Db 301 NPIIYAFGEKFRRLSVPRPKITKRPCKQCPVYFYRTDVGTSTNPSTGEQVSAGL 360

RESULT 5
 US-10-439-845-8

Sequence 8, Application US/10439845
 Publication No. US200301953348A1
 GENERAL INFORMATION:
 ; APPLICANT: Combadiere et al.; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
 ; TITLE OF INVENTION: AND THERAPEUTIC AGENTS FOR HIV INFECTION
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

RESULT 6
 US-10-741-601-285
 ; Sequence 285, Application US/10741601
 ; Publication No. US20040166519A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cargill, Michele et al.; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01500
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 26415
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 285
 ; LENGTH: 360
 ; TYPE: PRT

ORGANISM: Homo sapiens
US-10-741-601-285

Query Match 100.0%; Score 1900; DB 16; Length 360;
Best Local Similarity 100.0%; Pred. No. 4..5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRTRNTNESGEVTFFDYGAPCKFDYKQIGAQOLLPLSLYFIFGVGN 60
Db 1 MLSTSRSRTRNTNESGEVTFFDYGAPCKFDYKQIGAQOLLPLSLYFIFGVGN 60
Qy 61 MLVVLILINCKLKCLTDIYLNLAIASDLFLITLPIWAHSAANEWFGNAMCKLFGTGLY 120
Db 61 MLVVLILINCKLKCLTDIYLNLAIASDLFLITLPIWAHSAANEWFGNAMCKLFGTGLY 120
Qy 121 HIGYGG1FFFILLTIDRYLAIVHAVALKARTVTFGVTSVITWLVAEVSPGIFTK 180
Db 121 HIGYGG1FFFILLTIDRYLAIVHAVALKARTVTFGVTSVITWLVAEVSPGIFTK 180
Qy 181 CQEDSVTVCGPYPRGNNFHIMRNLLGVLPLIMIVCYSGILKLRLCRNECKRHR 240
Db 181 CQEDSVTVCGPYPRGNNFHIMRNLLGVLPLIMIVCYSGILKLRLCRNECKRHR 240
Qy 241 AYRVFTIMIVYFLWTPYNIVLNLNTQEFGLSNCESTSOLOQATQVTETLGMTHCCI 300
Db 241 AYRVFTIMIVYFLWTPYNIVLNLNTQEFGLSNCESTSOLOQATQVTETLGMTHCCI 300
Qy 301 NPIIYAFGEKPRYLSPVERKHITKPKCQCPVYFRETVDGYTSNTPSQEVSAGL 360
Db 301 NPIIYAFGEKPRYLSPVERKHITKPKCQCPVYFRETVDGYTSNTPSQEVSAGL 360

RESULT 7
US-10-741-601-286

; Sequence 286, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO011500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 286
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-741-601-286

Query Match 100.0%; Score 1900; DB 16; Length 360;
Best Local Similarity 100.0%; Pred. No. 4..5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRTRNTNESGEVTFFDYGAPCKFDYKQIGAQOLLPLSLYFIFGVGN 60
Db 1 MLSTSRSRTRNTNESGEVTFFDYGAPCKFDYKQIGAQOLLPLSLYFIFGVGN 60
Qy 61 MLVVLILINCKLKCLTDIYLNLAIASDLFLITLPIWAHSAANEWFGNAMCKLFGTGLY 120
Db 61 MLVVLILINCKLKCLTDIYLNLAIASDLFLITLPIWAHSAANEWFGNAMCKLFGTGLY 120
Qy 121 HIGYGG1FFFILLTIDRYLAIVHAVALKARTVTFGVTSVITWLVAEVSPGIFTK 180
Db 121 HIGYGG1FFFILLTIDRYLAIVHAVALKARTVTFGVTSVITWLVAEVSPGIFTK 180
Qy 181 CQEDSVTVCGPYPRGNNFHIMRNLLGVLPLIMIVCYSGILKLRLCRNECKRHR 240
Db 181 CQEDSVTVCGPYPRGNNFHIMRNLLGVLPLIMIVCYSGILKLRLCRNECKRHR 240
Qy 241 AYRVFTIMIVYFLWTPYNIVLNLNTQEFGLSNCESTSOLOQATQVTETLGMTHCCI 300

RESULT 8
US-10-791-592-4

; Sequence 4, Application US/10791592
; Publication No. US2004021964A1
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/791,592
; FILING DATE: 01-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/625,573
; FILING DATE: 25-TJul-2000
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Neely, Richard
; REGISTRATION NUMBER: 30,092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-843-5000
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 imino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
; US-10-791-592-4

Query Match 100.0%; Score 1900; DB 16; Length 360;
Best Local Similarity 100.0%; Pred. No. 4..5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRTRNTNESGEVTFFDYGAPCKFDYKQIGAQOLLPLSLYFIFGVGN 60
Db 1 MLSTSRSRTRNTNESGEVTFFDYGAPCKFDYKQIGAQOLLPLSLYFIFGVGN 60
Qy 61 MLVVLILINCKLKCLTDIYLNLAIASDLFLITLPIWAHSAANEWFGNAMCKLFGTGLY 120
Db 61 MLVVLILINCKLKCLTDIYLNLAIASDLFLITLPIWAHSAANEWFGNAMCKLFGTGLY 120
Qy 121 HIGYGG1FFFILLTIDRYLAIVHAVALKARTVTFGVTSVITWLVAEVSPGIFTK 180
Db 121 HIGYGG1FFFILLTIDRYLAIVHAVALKARTVTFGVTSVITWLVAEVSPGIFTK 180
Qy 181 CQEDSVTVCGPYPRGNNFHIMRNLLGVLPLIMIVCYSGILKLRLCRNECKRHR 240
Db 181 CQEDSVTVCGPYPRGNNFHIMRNLLGVLPLIMIVCYSGILKLRLCRNECKRHR 240
Qy 241 AYRVFTIMIVYFLWTPYNIVLNLNTQEFGLSNCESTSOLOQATQVTETLGMTHCCI 300

RESULT 9
 US-10-791-166-4 Application US/10791166
 ; Publication No. US2004023968A1

GENERAL INFORMATION:
 APPLICANT: Charo, Israel
 Coughlin, Shawn
 TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT PROTEIN RECEPTORS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooley Godward Castro Huddleston & Tatum
 STREET: 5 Palo Alto Square
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94106-2155

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/791,166
 FILING DATE: 01-Mar-2004
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/625,573
 FILING DATE: 25-Jul-2000
 APPLICATION NUMBER: US/08/446,669
 FILING DATE: May 25, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Neely, Richard
 REGISTRATION NUMBER: 30,092
 REFERENCE/DOCKET NUMBER: UCAL-237/01US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-5000
 TELEX: 38016cooleypa

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 360 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-791-166-4

RESULT 10
 US-10-700-313-8
 ; Sequence 8, Application US/10700313
 ; Publication No. US20040259785A1

GENERAL INFORMATION:
 APPLICANT: Combadiere et al.,
 TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
 NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
 ADDRESS: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/700,313
 FILING DATE: 31-Oct-2003
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/064,458
 FILING DATE: 8-MAY-1997
 APPLICATION NUMBER: Provisional 60/018,508
 FILING DATE: May 28, 1996

ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 08830/030001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 360 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-700-313-8

Query Match Score 1900; DB 16; Length 360;
 Best Local Similarity 100.0%; Pred. No. 4.5e-150; Length 360;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRIRNTNESGEVTTFDYDGAPECHKFDFKIGAQOLLPLYSLYFIFGVGN 60
 Db 1 MLSTSRSRIRNTNESGEVTTFDYDGAPECHKFDFKIGAQOLLPLYSLYFIFGVGN 60
 Qy 61 MLVYLILINCKLKCLDIYLLNIAISDLFLITLPLWAHSAANEWFGNACKLFGLY 120
 Db 61 MLVYLILINCKLKCLDIYLLNIAISDLFLITLPLWAHSAANEWFGNACKLFGLY 120
 Qy 121 HIGYFGGIFFIILITIDRYLAIVHAFALKARTVTGFVTSVITWLAVFASVPGIIFTK 180

Qy 181 CQKEDSVTVCGPYPRGRNNFFTMRNLTGVLVPLLINVICYSGILKTLRCNEKGRHR 240
 Qy 241 AVRVIPTIMIVYFLEWTPTNVILLNTQEPFGISNCESTSOLDQATQVTEIGMTHCCCI 300
 Db 241 AVRVIPTIMIVYFLEWTPTNVILLNTQEPFGISNCESTSOLDQATQVTEIGMTHCCCI 300
 Qy 301 NPIIYAFGEKFRYLSVFRRKHTKRFCKQCPVYFRETVDGVTSINTPSTGEQEVAGL 360
 Db 301 NPIIYAFGEKFRYLSVFRRKHTKRFCKQCPVYFRETVDGVTSINTPSTGEQEVAGL 360
 Qy 301 NPIIYAFGEKFRYLSVFRRKHTKRFCKQCPVYFRETVDGVTSINTPSTGEQEVAGL 360
 Db 301 NPIIYAFGEKFRYLSVFRRKHTKRFCKQCPVYFRETVDGVTSINTPSTGEQEVAGL 360

Db 121 HIGYFGGIFPFLITIDRYLAIVHAFALKARTVTGFVTTVITWLVAVFASPGIFTK 180
 Qy 181 CQEDSVTVCGPYPRGHNNFTIMRNILGVLPLIMIVCYSGILKTLRCRNEKRRHR 240
 Db 181 CQEDSVTVCGPYPRGHNNFTIMRNILGVLPLIMIVCYSGILKTLRCRNEKRRHR 240
 Qy 241 AYVIFTIMIVYLFWTYPNIVILLNTQEFGLSNCESTSOLIDATOATQVTTLGTMTHCC 300
 Db 241 AYVIFTIMIVYLFWTYPNIVILLNTQEFGLSNCESTSOLIDATOATQVTTLGTMTHCC 300
 Qy 301 NPIYAFGEKFRRLSYFFRKHITKRCKQCPVYRETVDGVTSINTTPSTGEOEVSAGL 360
 Db 301 NPIYAFGEKFRRLSYFFRKHITKRCKQCPVYRETVDGVTSINTTPSTGEOEVSAGL 360

RESULT 11
 US-10-486-471-4
 ; Sequence 4, Application US/10486471
 ; Publication No. US20050101530A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TOPGEN PHARMACEUTIQUE INC.
 ; TITLE OF INVENTION: CELLULAR VIRUS RECEPTORS AND METHODS OF USE
 ; FILE REFERENCE: 009853-0003
 ; CURRENT APPLICATION NUMBER: US/10/486,471
 ; PRIORITY APPLICATION NUMBER: US/10/486,471
 ; FILING DATE: 2004-02-10
 ; PRIOR PRIORITY DATE: 2001-08-10
 ; NUMBER OF SEQ ID NO: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 360
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-486-471-4

Query Match 100.0%; Score 1900; DB 17; Length 360;
 Best Local Similarity 100.0%; Pred. No. 4.5e-150;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRIRNTNESGEVTTFDYDGA^PCHKFVKQIGOLLPLPLSIVL^FFGVGN 60
 Db 1 MLSTSRSRIRNTNESGEVTTFDYDGA^PCHKFVKQIGOLLPLPLSIVL^FFGVGN 60
 Qy 61 MLVVLILINCKKLCKLTDIYLNLIAISDLFLITLPWAHSANNEWFGNAMCKLIFTGLY 120
 Db 61 MLVVLILINCKKLCKLTDIYLNLIAISDLFLITLPWAHSANNEWFGNAMCKLIFTGLY 120
 Qy 121 HIGYFGGIFPFLITIDRYLAIVHAFALKARTVTGFVTTVITWLVAVFASPGIFTK 180
 Db 121 HIGYFGGIFPFLITIDRYLAIVHAFALKARTVTGFVTTVITWLVAVFASPGIFTK 180
 Qy 181 CQEDSVTVCGPYPRGHNNFTIMRNILGVLPLIMIVCYSGILKTLRCRNEKRRHR 240
 Db 181 CQEDSVTVCGPYPRGHNNFTIMRNILGVLPLIMIVCYSGILKTLRCRNEKRRHR 240
 Qy 241 AYVIFTIMIVYLFWTYPNIVILLNTQEFGLSNCESTSOLIDATOATQVTTLGTMTHCC 300
 Db 241 AYVIFTIMIVYLFWTYPNIVILLNTQEFGLSNCESTSOLIDATOATQVTTLGTMTHCC 300
 Qy 301 NPIYAFGEKFRRLSYFFRKHITKRCKQCPVYRETVDGVTSINTTPSTGEOEVSAGL 360
 Db 301 NPIYAFGEKFRRLSYFFRKHITKRCKQCPVYRETVDGVTSINTTPSTGEOEVSAGL 360

RESULT 12
 US-10-846-185-8
 ; Sequence 8, Application US/10846185
 ; Publication No. US20050118677A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Combadiere et al.,
 ; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELLS
 ; NUMBER OF SEQUENCES: 9

RESULT 13
 US-09-131-827A-20
 ; Sequence 20, Application US/09131827A
 ; Patent No. US2002038469A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dean, Michael
 ; APPLICANT: O'Brien, Stephen J.

; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; FILE REFERENCE: 14014_0333
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; CURRENT APPLICATION NUMBER: US/09/131,827A
; PRIOR APPLICATION NUMBER: 1998-08-10
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-131-827A-20

Query Match 99.9%; Score 1899; DB 9; Length 360;
Best Local Similarity 99.7%; Pred. No. 5.e-150;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSPRINTNESGEVTFFDYDGAPECHKFDYKQIGAQOLLPLPLSVPYIIFGFGVN 60
Db 1 MLSTSRSPRINTNESGEVTFFDYDGAPECHKFDYKQIGAQOLLPLPLSVPYIIFGFGVN 60

Qy 61 MLVVLILINCKKLKCLTDIYLNLAISDLFLITLTDYLAIVHAFALKARTVTFGVUTSVTMLAVFAVS PGIIPTK 120
Db 61 MLVVLILINCKKLKCLTDIYLNLAISDLFLITLTDYLAIVHAFALKARTVTFGVUTSVTMLAVFAVS PGIIPTK 120

Qy 121 HIGYFGG1FPIIILTIDYLAIVHAFALKARTVTFGVUTSVTMLAVFAVS PGIIPTK 180
Db 121 HIGYFGG1FPIIILTIDYLAIVHAFALKARTVTFGVUTSVTMLAVFAVS PGIIPTK 180

Qy 181 COKESDTVVCGPYPPRGNNFTIMRNLTGLVPLLMIVCYSGILKTLLRCNEKGRHR 240
Db 181 COKESDTVVCGPYPPRGNNFTIMRNLTGLVPLLMIVCYSGILKTLLRCNEKGRHR 240

Query Match 99.9%; Score 1899; DB 9; Length 360;
Best Local Similarity 99.7%; Pred. No. 5.e-150;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSPRINTNESGEVTFFDYDGAPECHKFDYKQIGAQOLLPLPLSVPYIIFGFGVN 60
Db 1 MLSTSRSPRINTNESGEVTFFDYDGAPECHKFDYKQIGAQOLLPLPLSVPYIIFGFGVN 60

Qy 61 MLVVLILINCKKLKCLTDIYLNLAISDLFLITLTDYLAIVHAFALKARTVTFGVUTSVTMLAVFAVS PGIIPTK 120
Db 61 MLVVLILINCKKLKCLTDIYLNLAISDLFLITLTDYLAIVHAFALKARTVTFGVUTSVTMLAVFAVS PGIIPTK 120

RESULT 15
US-10-925-095-473
; Sequence 473, Application US/10/925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.,
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SEQ ID NO 473
; SOFTWARE: PatentIn Version 2.1
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-925-095-473

Query Match 99.7%; Score 1894; DB 17; Length 360;
Best Local Similarity 99.7%; Pred. No. 1.e-149;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLSTSRSPRINTNESGEVTFFDYDGAPECHKFDYKQIGAQOLLPLPLSVPYIIFGFGVN 60
Db 1 MLSTSRSPRINTNESGEVTFFDYDGAPECHKFDYKQIGAQOLLPLPLSVPYIIFGFGVN 60

Qy 61 MLVVLILINCKKLKCLTDIYLNLAISDLFLITLTDYLAIVHAFALKARTVTFGVUTSVTMLAVFAVS PGIIPTK 120
Db 61 MLVVLILINCKKLKCLTDIYLNLAISDLFLITLTDYLAIVHAFALKARTVTFGVUTSVTMLAVFAVS PGIIPTK 120

Qy 121 HIGYFGG1FPIIILTIDYLAIVHAFALKARTVTFGVUTSVTMLAVFAVS PGIIPTK 180
Db 121 HIGYFGG1FPIIILTIDYLAIVHAFALKARTVTFGVUTSVTMLAVFAVS PGIIPTK 180

Query Match 99.7%; Score 1894; DB 10; Length 360;
Best Local Similarity 99.7%; Pred. No. 1.e-149;
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non- Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 589
; SEQ ID NO 473
; SOFTWARE: PatentIn Version 2.1
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-826-509-473
; Sequence 473, Application US/09/826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non- Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SEQ ID NO 473
; SOFTWARE: PatentIn Version 2.1
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-826-509-473
Query Match 99.7%; Score 1894; DB 10; Length 360;
Best Local Similarity 99.7%; Pred. No. 1.e-149;

Qy	241	AVRIFTIMIVIFLFWTPYNIVILLNTFQEFFGLSNCESTISOLDQATOVTETLGMTHCCI	300
Db	241	AKRIFTIMIVIFLFWTPYNIVILLNTFQEFFGLSNCESTISOLDQATOVTETLGMTHCCI	300
Qy	301	NPIIYAFGEKFRRLSVFRKHITKRFCKQQCPVYFYRETVDGVTSINTPSTGEQEVSAGL	360
Db	301	NPIIYAFGEKFRRLSVFRKHITKRFCKQQCPVYFYRETVDGVTSINTPSTGEQEVSAGL	360

Search completed: June 9, 2005, 17:06:38
Job time : 101.545 secs